

[illegible]

Db	1461	CCTGCTCAACCCGGACTTCGGCCCTCTCGCGGAAGTATCGGCTTCCACGGAGCCAAAGT	1520
QY	1838	CACCGATCCGAAGAAAGTTCCCGACGACGCTAGCTGAGGCAATATCTGGACCTGT	1897
Db	1521	GACCGCGCTCGAGGAGCTCGACGAGCGGCTGCAGGAATTCCTCCGCCACGCCGCTCGGC	1580
QY	1898	ACTGATGATATTCCTCAAGGATCCTTAATGGCGCTGCATCCACCAACCATCAGTGGGA	1957
Db	1581	GCTGCTGGACCTGCATACCAACCTCGGAGACTGTATGCCGCGGAATCGAGTTGCG	1640
QY	1958	ACAGSTC	1964
Db	1641	CCAGSTC	1647

```

1      RESULT 2
2      US-09-252-991A-7413
3      ; Sequence 7413, Application US/09252991A
4      ; Patent No. 6531795
5      ; GENERAL INFORMATION:
6      ; APPLICANT: Marc J. Rubenfield et al.
7      ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
8      ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
9      ; FILE REFERENCE: 107196.136
10     ; CURRENT APPLICATION NUMBER: US/09/252,991A
11     ; CURRENT FILING DATE: 1999-02-18
12     ; PRIOR APPLICATION NUMBER: US 60/074,788
13     ; PRIOR FILING DATE: 1998-02-18
14     ; PRIOR APPLICATION NUMBER: US 60/094,190
15     ; PRIOR FILING DATE: 1998-07-27
16     ; NUMBER OF SEQ ID NOS: 33142
17     ; SEQ ID NO 7413
18     ; LENGTH: 1083
19     ; TYPE: DNA
20     ; ORGANISM: Pseudomonas aeruginosa
21     US-09-252-991A-7413

```

Query Match	7.6%	Score 164.2	DB 4	Length 1083
Best Local Similarly	50.9%	Pred. No. 5.2e-41		
Matches 469	Conservative	0	Mismatches 443	Indels 9
				Gaps 3

QY 341 GCAGAACAAATTAATTGCACTTGTGGAAAGCTCAAGAGTGTGAAGGCAATTTTGGTTGGT 400
 Db 42 CGCCGAGATGCTGCTGGAAACCTTGGANAGCCGCCGCGCTCCGCCATTGCTATGGCATTGT 101
 QY 401 GGGTGACAGCCTTAATCCGATCGTGGATGCTGTCCGCCAATCAGATATTGAGTGGGTGCA 460
 Db 102 CGGCGACACCCCTCAACCATTGTCCACGAGCCCATCATGTGACGACAGATCCAGTGGGTGCA 161
 QY 461 CCTTCGAATATAGAAAGCGCGGGCGTTTGCAGCCGGTGTCCGGAATCGTTGATCACTAGGGGA 520
 Db 162 CGTGGCCACAGAAAGCGCGGCCCTTCGCCGCGGGGCCGAGTCATACATCACCGGACG 221
 QY 521 GCTGCACTATGTGCTGCTTTGTGTGTGCTCTGGAACACACACCTGATTACAGGCTCTTA 580
 Db 222 CCTGACGCGCTGCGCGGCTCTCTCGGAGCGGGCAGCCTGCATCTTCATCAAGGGCGTGA 281
 QY 581 TGATTGCGATCGAAATGCTGCGAAGGTGTGGCATGCGTACGATATTCGGAATGCCCA 640
 Db 282 CGAGGCCACGAGCAACCGCGCGGATGTGCTATGCGCCAGCCAGATCGTTACCCGCGCA 341
 QY 641 GATTGGTGCAGCTTCTTCGAGGAAGCAATCCGAGATTTGTTTAAGAAATGCTGTGG 700
 Db 342 ACTGGGCAATGAGATTTCGCCAGAGGTGTCGACTTAAAGCGGCTCTTAGCCAGAGCTGTGGT 401
 QY 701 TTACTGCGAGATGAGTGTGATGTGTGAGACAGGTGAAGCAATTTTGCATCAAGGATATCA 760
 Db 402 GTTTCGCGAGAGGTGACACAGCCCGGAACAGGCGCGCGGTGTGGTGGCCCTGGCTGCA 461
 QY 761 GTCCACCATGGCGGGTAAAGGTGTGTGTGTGTGTATGATTTCTGTGTATATCCGCTAAGA 820
 Db 462 GGGCGCGCTCAACCGGGCGCGCGGTGGGTGTATCCTGTGCGCCGCGCATAC---GACC 517

[illegible][illegible]

Db 1823 -----GCGCGCGCGGCTGAGCGGCGGTGACGGCCAGTCCGAGGAAGCCGCGCG 1875
QY 1377 CATAAGTCGAGAACAGCATGTGCTATTCACCTGATACGTTGCTCTATTTTGAACGAG 1436
Db 1876 CAGGCCGAGAACCCAGCCGACCCGATCAACCCGAGCGGGTATTCGTTCTCTGTCGAG 1935
QY 1437 CTGGCGGATTAAGATGCGGTGTTTACTGTGATACCGCATGGCAATGTGGCATGGG 1496
Db 1936 CAACATGCCGAGCATGCGATTTCTGCGCGCGACAGCGGCTCCGATACCACTGTGTACGCC 1995
QY 1497 AGGTACATCGAGAAATCCGAGGAAACGCGCATTTGTGGTTTCAATCCGCGACGACG 1556
Db 1996 CCGCAGATCCGATCCGCGCGCGCATGCTCGGCTCGCTG---TCGGGCAAGGTGGGAGAC 2052
QY 1557 ATGGCTAATGCGTTCCTCATGCGATTTGGTGGCAAGTGTGATCGAACCAGCAGTG 1616
Db 2053 ATGGCAGAGCGGTGCTCCCTACCGCATTCGCGCGCAAGCTCGCTATCCGAGCGGCGGTG 2112
QY 1617 ATCGGAGATGTGTGGGATGTGGTGGATGCTGTGGTGGAGCTTGTGACCGTTAG 1676
Db 2113 GTGGCGATGTGTGGGAGCGCGCCCATGCAATGAACGCGACCGCAACTGTGACCGTTAG 2172
QY 1677 CTGCACCACTTCCG-----TGAAGGCTGTGTGTTTAAACAAGT 1718
Db 2173 CAGCAGTACTGCGCAGCGCTGGGACTCGCCGACCTTCATCGTGTGTGTAACAACGCGC 2232
QY 1719 TCTTTGGGCGATGTGAAGTTGGAGATG---TCGTGAGAGGAGACCGCAATTTGTACT 1775
Db 2233 GATCTCAACCCAGGTGACCTGGAGCAGCGTGCCTCGCGCGGACCGGAGTTCAAGCCG 2292
QY 1776 GACCATGAGGAAGTGAATTTGCGAGAG-----ATTGGCGGCGGTGCGGTTTCAAAATG 1829
Db 2293 GCGCGAGAAGTGATGATTTCCCTACGCGGCTTATGGGACATGCTGCGCTTCAAGGCG 2352
QY 1830 GTAGCATCACCAGATCCGAAGAAGTTCGAGAGCTAGAGCATTTGGCATATCT 1889
Db 2353 ATCCGCGTGAATCCGCGAGACATCGACCGCGCTGGCGAGGCTTGGCGCGCGAC 2412
QY 1890 GGACCTGACTGATGATATGTCACGAGATCTATGCTGTGATCCACCAACCATC 1949
Db 2413 CGCCCGGTGCTGTGGAGGTGTACCGACCCGAAACGTCCGCGCTGCCCGCACATC 2472
QY 1950 ACGTGGAAACAGGTATG 1967
Db 2473 AGTTTCGAGCAGGCCAAG 2490

RESULT 8

US-09-252-991A-8530
; Sequence 8530, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 3142
; SEQ ID NO 8530
; LENGTH: 2754
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-8530

Query Match

4.6%; Score 100.4; DB 4; Length 2754;

Best Local Similarity 45.5%; Pred. NO. 7.2e-21;
Matches 773; Conservative 0; Mismatches 856; Indels 69; Gaps 9;

QY 327 ATGGCACACAGCTACCGACACAATTAATTGACACTTTGGAAGCTCAAGCTGTGAACGA 386
Db 671 ATGTCCAGACAGGTTGCTCCCATTAATGCTGAACCGCTTGAGCCAGTGGGGGTAACCGC 730
QY 387 ATTTATGTTTGGTGGGTGACACCTTAATCCATGCTGTGATGCTG-----CGCCAA 440
Db 731 GTCTTGGGCTACCCAGCCGACATGCAACAGGATATGGGCCATATGGCCCGCGCGCC 790
QY 441 TCAGATATTGAGTGGGTGACGTTTCAAAATGGAAGCGCGGCGTTTGCAGCGCGCGC 500
Db 791 GAGGATTTGACTATATCCCGCTGCGCCACAGAGAGATGGCGGCTTCATGCGCGCGCC 850
QY 501 GAATCGTATATCACTGGGAGCTGGCAGTATGCTGCTTCTTGTGCTCTGGAACACA 560
Db 851 CAGCGCAAGTTCAACCGAGAGGTCGGGCTGCTCGCCACCTCGGGGCGCGCGCATC 910
QY 561 CACCTGATTCAGGCTTTATATGTTGGATTCGAAATGTGCGAAGTGTGGCCATCGT 620
Db 911 CACCTGCTAAGCGGCTTACGACGCGCGCATGATCATCAGCGGCTGCGCATCTGC 970
QY 621 ACCCATATTCGAGTCCCGAGATTGCTGACGTTCTCCAGGAACCGCATCCGAGATT 680
Db 971 GGCGACAGCGGCTACCGCGTTGGCGACGACTACGACGAGAAATGCTGTGCAAGC 1030
QY 681 TTGTTTAAGGAATGCTCTGTTTACTGCGAGATGTGAATGTGTGAGCAGGCTGAACGC 740
Db 1031 TTGTTCAAGAGCTTTCGCTATGTCGAGACCGTGTGACCGCCGACACATGCTCAT 1090
QY 741 ATTTTGCATCAGCGCATTTAGTTCACATAGCGCGGTTAAAGTGTGTGCTGTGATGATT 800
Db 1091 GTGTGAGACCGACCTTGCGCTGGGCTGGGAGCGGAGCTGCGACGCTGAGATCGTG 1150
QY 801 CCTGTGATATGCTAAGSAGAACGC-----AGGTACGGTACTTATTCATTTCCACTAT 856
Db 1151 CCCAAGAGTGCACACAGATGGCGGCGCCGAGAGCGCCAGCCACCGACGACGCGACGTG 1210
QY 857 TTCTTCTGCACTCTGTGTGTCTCCGATCTA-----CTGAGGCTGCACG 905
Db 1211 ATGTGCGGCTGGGCTGTGTCACCGCAGCACTTACGCGCGCGACCGACCTCGAGGCGC 1270
QY 906 CTGTGTGAGGCGCATTAACACCGCTAAGTGTGACCTTTTGTGCGGTGCGGCGGTGAAG 965
Db 1271 GCGCGGGGATCTTAATGCGCGCGCGGCGGAGTCTTGCAGGTGCGCGCGCTCG 1330
QY 966 AATGCTCGCGCGCAGGTGTGAGTGTGCGGAGAAATTAATCAACCGATCGGCGCATGCG 1025
Db 1331 GCGCGGCAACCGCACTGGAACCGGTCCCGGAGCGCTGCGCGGAGTGGCCAAAGCGC 1390
QY 1026 CTGGGTGTAGCAGTACATCCAGCATGAAGATCCGTTGAGGTGCGCATGTCGTGCGCTG 1085
Db 1391 CTCTGTGGCAAGCGCGGCTTCCGACACACCTGCGTACGTGACCGGCTCCATCGGCGCTG 1450
QY 1086 CTGTGTACGGGCGCTGTGTGATGCGTCCATGAGGGGATCTGCTATTTATTTGGGT 1145
Db 1451 CTGGCACCGCGCGCAGCAGATGCTGATGAGGCAATTCGACACCCCTGTGATCTGCGC 1510
QY 1146 ACGATTTCCCTTATTCATTTCTCTTAAGACAAGTGTGCCAGGTGATATCAAC 1205
Db 1511 AGCACTTCCCTACAGGAGTCTCTACCGAAGCGCGCGCAGGCGGCGGTGACAGATC 1570
QY 1206 GGTGCG-----CACATTGTGACATCCACGAGTGAAGTATCCGCTGACCGGTAT 1256
Db 1571 GACCTGTATCCGCGCAGCATGCTATCCGATTCGATCGACAGGCGCTGTGTCGGCAT 1630
QY 1257 GTTGTGCAACATCGAATAATTTTGTGCTATGTGAAGGAAAAACAGATCTGCTCTTC 1316
Db 1631 CAGAGGAAACCTCTGAGCGCGCTGCTGCTGCTGCGAGCAAGAAAAACAGCGCGCT-- 1688
QY 1317 CTTATCGGATGCTCAAGCGACAGAGCGTAAAGTGAAGCTGCTGTGTGAGACATCAACA 1376
Db 1689 -----GCGCGCGCGGCTGACGCGGCGGTGAAGGCGCATGCGAGAGGAAGCCGCGCGC 1741

QY	1377	CATAACGTCGGAAGCAATGTCGCCAATTCACCTCAATACATGTTGGCTCATTTTAAACAG	1436
Db	1742	CAGCGCCGAAGAGCCACGCCACCCGATCAACCCGACGGGATTTCCGTTCCGAG	1801
QY	1437	CTGCGCGATAAGATGCGCGTGTATTACTGTGGATACCGGATGTCGAATGTTGGCATGCG	1496
Db	1802	CACCTGCCGAGCATGATTCGATTCCTCGCGGCCACAGCGGCTTGCAATACCACTGTTACGCC	1861
QY	1497	AGTATCATCCGAATCCGGAGGAAACGCGGACTTTGTGGTTCAATTCGCCACGGACG	1556
Db	1862	CGCGACATCCCAATGCGCGCGGGCATGCTCGGCTCGCTG---TCGGGCAAGCTGGCACC	1918
QY	1557	ATGGCTAATGCGTTCCTCATGCGATGTTGTCGCAAAAGTTGATTCGAACCCGACAGT	1616
Db	1919	ATGGGACAGCGCGCTGCCCCATCGCCATCGCCCAAGTCTGCTATTCGCGACGGCGCGG	1978
QY	1617	ATCGCGATGTGTGCGATGTGTGTGGGATGCTGCTGCGGTGAGCTTCTGACCGTTAAG	1676
Db	1979	GTGCGCATGTGTCGGCGGACGGCGCCATGACATGAACGGCAACGCCGAATGTCACCGTG	2038
QY	1677	CTGACCAACACTCCGC-----TGAAAGCTGTGGTGTTTAAACACAGT	1718
Db	2039	CAGCAGTATCTGCGCAGCGCTGGGACTCGCCGCACTTCAATCGTCTGTGTGTAACACGGC	2098
QY	1719	TCTTTGGGCATGTGTAAGTTGGAGATGC---TCGTGGAGGGACACGACGAATTTGGTACT	1775
Db	2099	GATCTCAACCGAGTGACCTGGGACACAGTGCCTGCGCGGACGCCGGAGTTACGCCG	2158
QY	1776	GACCATGAGGAAGATTTCCGAGAG-----ATTGCGCGGCTGCGGGTATTCAAATCG	1829
Db	2159	GGCGAGGAAGATGATTCATTTCCCTACGCGCGTTATCGACATGCTCGGCTTCAAGGGC	2218
QY	1830	GTACGCATCAACCGATCCGGAAGATTCGCGAGCAGTACTGAGGATGGGATATGCT	1889
Db	2219	ATCCGCGTGATTCGCCGAGAGCATATGAGCGCGCCCTGGGCCGAGAGCTTTCGCCCGCAG	2278
QY	1890	GGACCTTACTGATCGATATCGATCGACGATCCTTAATCGCTGTGATCCGACCAACATC	1949
Db	2279	CGCCCGGTGTCTGCGAGGTGTCTACCGACCCGACAGTGCCTCGCGCTGCCGCGCATC	2338
QY	1950	ACGTGGGACAGAGTCAATC	1967
Db	2339	AGTTGAGCAGCGCCAG	2356
RESULT 9			
US-08-735-545-24/c			
: Sequence 24, Application US/08735545			
: Patent No. 6025131			
: GENERAL INFORMATION:			
: APPLICANT: Van Dyk, Tina K.			
: APPLICANT: Larossa, Robert Alan			
: TITLE OF INVENTION: A Facile Method for			
: TITLE OF INVENTION: Identifying Regulated			
: NUMBER OF SEQUENCES: 28			
: CORRESPONDENCE ADDRESS:			
: ADDRESSEE: E. I. DU PONT DE NEMOURS			
: ADDRESSEE: AND COMPANY			
: STREET: 1007 MARKET STREET			
: CITY: WILMINGTON			
: STATE: DELAWARE			
: COUNTRY: UNITED STATES OF AMERICA			
: ZIP: 19898			
: COMPUTER READABLE FORM:			
: MEDIUM TYPE: DISKETTE, 3.50 INCH			
: COMPUTER: IBM PC COMPATIBLE			
: OPERATING SYSTEM: MICROSOFT WINDOWS 3.1			
: SOFTWARE: MICROSOFT WORD 2.0C			
: CURRENT APPLICATION DATA:			
: APPLICATION NUMBER: US/08/735,545			
: FILING DATE:			
: CLASSIFICATION:			

ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA A.
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CR-99899
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-8112
TELEFAX: 302-773-0164
INFORMATION FOR SEO ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 260 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: dpd3509 lower

QY	471	TAGGAAGGGGGGGTTTGGACGCGGTGCGGAATGCTTGATCTAGTGGGAGAGCTGGGACAGTA	520
Db	260	GAAGAAGGGGGGGCTTTGCCGCTGCGCTTGAGACACACTTACGCGAAGACCTGGCGGTG	201
QY	531	TGTGCTGCTTCTTGTGTGTCTGGAAACACACACTGATTACAGGGTCTTTATGATTGCAAT	590
Db	200	TGCCCGGATGCTGCGGCCCCGGCACCTGACCTTAATCAACAGGCGCTGTTGCATTGCCAC	141
QY	591	CGAATAGTGGGAAGGTGTGGCCATGCTTACCCATATTCCGATGAGTGGCCAGATTGTTGG	650
Db	140	CGCAATACGTTCCGGTACTGGCGATTGCCGCTCATATTCCCTCCAGCGAATAATTGGCAGC	81
QY	651	ACGTTCTTCCAGGAACGCAATCCGAGATTTTGTATGAAGATGCTGTGTTACTGCGAG	710
Db	80	GGCTATTTCGAGGAACCCACCACAAAGACTATTCCCGCAATGTAGTACATATTGCCAG	21
QY	711	ATGCTGAATGTTGGTGAACA	730
Db	20	CTGTGTTCCAGCCCGGAGACA	1

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1      RESULT 12
2      US-08-452-075-1
3      ; Sequence 1, Application US/08452075
4      ; Patent No. 598178
5      ;
6      ; GENERAL INFORMATION:
7      ;
8      ; APPLICANT: HASHIGUCHI, KEN-ICHI
9      ; APPLICANT: KISHINO, HIROKO
10     ; APPLICANT: TSUTSUMOTO, NOBUHARU
11     ; APPLICANT: MATSUI, HIROSHI
12     ; TITLE OF INVENTION: L-ISOLEUCINE-PRODUCING BACTERIUM AND
13     ; TITLE OF INVENTION: METHOD FOR PREPARING L-ISOLEUCINE THROUGH FERMENTATION
14     ; NUMBER OF SEQUENCES: 9
15     ; CORRESPONDENCE ADDRESS:
16     ; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT
17     ; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
18     ; CITY: ARLINGTON
19     ; STATE: VIRGINIA
20     ; COUNTRY: USA
21     ; ZIP: 22202
22     ;
23     ; COMPUTER READABLE FORM:
24     ; MEDIUM TYPE: Floppy disk
25     ; COMPUTER: IBM PC compatible
26     ; OPERATING SYSTEM: PC-DOS/MS-DOS
27     ; SOFTWARE: Patent In Release #1.0, Version #1.30
28     ; CURRENT APPLICATION DATA:
29     ; APPLICATION NUMBER: US/08/452,075
30     ; FILING DATE: 26-MAY-1995
31     ; CLASSIFICATION: 435
32     ;
33     ; PRIOR APPLICATION DATA:
34     ; APPLICATION NUMBER: JP 116340/1994
35     ; FILING DATE: 30-MAY-1994
36     ; ATTORNEY/AGENT INFORMATION:
37     ; NAME: OBLON, NORMAN F
38     ; REGISTRATION NUMBER: 08/452,075
39     ; REFERENCE/DOCKET NUMBER: 10-741-0
40     ; TELECOMMUNICATION INFORMATION:
41     ; TELEPHONE: (703) 413-3000
42     ; TELEFAX: (703) 413-2220
43     ; TELEX: 248855 OPAT UR
44     ; INFORMATION FOR SEQ ID NO: 1:
45     ; SEQUENCE CHARACTERISTICS:
46     ; LENGTH: 2841 base pairs
47     ; TYPE: nucleic acid
48     ; STRANDEDNESS: double
49     ; TOPOLOGY: linear
50     ; MOLECULE TYPE: DNA (genomic)
51     ; FEATURE:
52     ; NAME/KEY: CDS
53     ; LOCATION: 957..1052
54     ; FEATURE:

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NAME/KEY: CDS
LOCATION: 1195..2838
US-08-452-075-1

Query Match 2.8%; Score 60.8; DB 2; Length 2841;
Best Local Similarity 45.8%; Pred. No. 1.7e-08;
Matches 209; Conservative 0; Mismatches 247; Indels 0; Gaps 0;

341 CGCAGAACATTAATGACATTTGGAACCTCAAGTGTGAAGCAATTATGTTGGT 400
1203 CGCAGAGTGGTGTGATCGCTTGGGGCAGAGGTGTGAACACCGTTTGGTTATCC 1262
401 GGGTGACAGCTTAATCGATCGGTGGATCTCTCCGCAATGATATTAGTGGGTGCA 460
1263 GGGTGGCCGAATTAATCCGCTTACGATGATGATGACGGCGGCGTGAACCACTTGTCT 1322
461 CGTTGCAATGAGGAGCGCGCGCTTTCACACCGCTGCGAATGTTGATGACATCGGGA 520
1323 ATGCCACATGAGCAGAGGTGCGGCAATGCGGCTTATCGTTGCTCGCTACCGGCA 1382
521 GCTGAGATATGTGCTCTCTTGTGTCCTGGAACACACACCTGATTCAGGGTCTTTA 580
1383 AACTGGCATATGATGATCGCACGCTCTGTCGGGCGCAACCACTGATTAACGGGCTTGC 1442
581 TGATTCGATCGCAATGAGTGGCGAAGGTGTGGCCATCGCTACCATATTCGAGTCCCA 640
1443 GGACGCACTGTATGATTCATCCCTCTTGTTCATCACCCTGTAAGTTCGACACCTTT 1502
641 GATTGTTGACCTTCTCCAGAAACGATCCGAGATTTGTTAAGAAATGCTCTGG 700
1503 TATCGGCACTGACGATTCAGAGAGTGAATGCTGCGATTTGCTTACCGTACCA 1562
701 TTACTGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 760
1563 GCATGACCTTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1622
761 GTCCACCATGCGCGGTAAGGTGTGCTGCTGATGATGATGATGATGATGATGATGATGAT 796
1623 CGTTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1658

RESULT 13
US-09-231-061-1
Sequence 1, Application US/09231061
Patent No. 6214591

GENERAL INFORMATION:
APPLICANT: TOMITA, FUSAO
APPLICANT: YOKOTA, ATSUSHI
APPLICANT: HASHIGUCHI, KENICHI
APPLICANT: ISHIGOKA, MASAKO
APPLICANT: KURAHASHI, OSAMU
TITLE OF INVENTION: METHODS FOR PRODUCING L-VALINE AND
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESS: OBLON, SPIVAK, MCCLELLAND, MATR & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. JEFF. DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/231,061
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/793,441

FILING DATE: 28-FEB-1997
APPLICATION NUMBER: PCT/JP95/01719
FILING DATE: 30-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-204856
FILING DATE: 30-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-843-0 PCT
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2841 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: ESCHERICHIA COLI
STRAIN: M162
FEATURE:
NAME/KEY: CDS
LOCATION: 957..1055
OTHER INFORMATION: /note= "IDENTIFICATION METHOD: S"
FEATURE:
NAME/KEY: attenuator
LOCATION: 1081..1104
OTHER INFORMATION: /note= "IDENTIFICATION METHOD: S"
FEATURE:
NAME/KEY: CDS
LOCATION: 1195..2841
OTHER INFORMATION: /note= "IDENTIFICATION METHOD: S"
FEATURE:
NAME/KEY: misc-feature
LOCATION: 52..57
OTHER INFORMATION: /note= "CLEAVAGE SITE: SmaI,
OTHER INFORMATION: IDENTIFICATION METHOD: S"
FEATURE:
NAME/KEY: misc-feature
LOCATION: 2395..2400
OTHER INFORMATION: /note= "CLEAVAGE SITE: KpnI,
OTHER INFORMATION: IDENTIFICATION METHOD: S"

Query Match 2.8%; Score 60.8; DB 3; Length 2841;
Best Local Similarity 45.8%; Pred. No. 1.7e-08;
Matches 209; Conservative 0; Mismatches 247; Indels 0; Gaps 0;

341 CGCAGAACATTAATGACATTTGGAAGCTCAAGGTGTGAAGCAATTATGTTGGT 400
1203 CGCAGAGTGGTGTGATCGCTTGGGGCAGAGGTGTGAACACCGTTTGGTTATCC 1262
401 GGGTGACAGCTTAATCGATCGGTGGATCTCTCCGCAATGATATTAGTGGGTGCA 460
1263 GGGTGGCCGAATTAATCCGCTTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 760
1563 GCATGACCTTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1622
761 GTCCACCATGCGCGGTAAGGTGTGCTGCTGATGATGATGATGATGATGATGATGATGAT 796
1623 CGTTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1658


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Db 6317 AAGTTCGCCACGAAAGACAGGTGCTCTTGCACGCGGTATGCAAGCTAAATTGCGCGCT 6258
QY 520 AGCTGGCAGTATGTGCTGCTCTTGTGTCCTGGAACACACACCTGATTCAGGGTCTT 579
Db 6257 CAATCGGGGTGTGAGTTGTTCCAGTGTGTCAGGTGCGACTGACTGATTAACGGTGT 6198
QY 580 ATGATTGCGATCGAAATGTGCGAAGGTGTGGCCATGCGCTAGCCATATTCGAGTCCC 639
Db 6197 ACGATGCACTTATGATTAACACTCCATTCCTAGCGATCCTTGATCAGCTCCAGTTAACG 6138
QY 640 AGATTGCTGCACTCTTCCAGAAACGATCCGGAGATTTGTTAAGSAATGCTCTG 699
Db 6137 AATTGAACATGATGCTTTCACAGAGCTTAACCAAAACCAATGTACAAAGGTATGCTG 6078
QY 700 GTTACTGCGAGATGTGAATGTGTGAGCAGGAGTGACGATTTGCAATCAAGCGATTC 759
Db 6077 TTACACAAACGTTAGCTTACGTAGAGCAATTGCCAAAGTAATTGACGAAGCCTGCC 6018
QY 760 AGTCCACCATGGCGGGTAAAGTGTGTGCTGATGATTCCTGATATGCTAAGG 819
Db 6017 GTGCTGCAAGTTCTTAAAAAAGTCCAGCTGTGTGAAATTCACGTAACCTTGGTTCC 5958
QY 820 AAGACGAGGTGACGCTACTTATTCCAATTC 850
Db 5957 AAGAAATGATGAAGAACTCATCTACGTTTC 5927
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Search completed: October 3, 2003, 18:52:48
Job time : 164 secs

C glutamicum codin
Corynebacterium gl
C glutamicum pyru

Nucleotide sequence

Corynebacterium po

Propionibacterium
Salmonella typhi D

Corynebacterium po

Escherichia coli p

Corynebacterium gl

DNA encoding novel

Pathogen specific antibodies

Human ORFX polynuc

Listeria innocua

Bacillus licheniformis

C. glutamicum tran

mal nutrition;
ase; poxB.
Genomic sequence
E.coli promoter re
Sulfolobus methyl
C. glutamicum deri
Oligonucleotide fo

XX		/ Product -
PN	WO200168894-A1.	Enzyme Oxidase
XX		
PD	20-SEP-2001.	
XX		
PF	05-JUL-2000; 2000WO-EP06305.	
XX		
PR	17-MAR-2000; 2000US-0528196.	
XX		
PA	(DEGS) DEGUSA AG.	
XX	(DYNA-) UNIV NAT IRELAND.	
XX		

PI Dunleavy LK, McCormack A, Stapleton C, Burke K, Moeckel B:
PI Thierbach G.

XX
DR MPI: 2001-656800/75.
P-PSDB: AAU10194.

XX Preparation of L-lysine, e.g. L-lysine, L-threonine or
PT L-isoleucine, useful in animal nutrition or in human medicine,
PT comprises fermenting L-lysine acid-producing coryneform bacteria with
PT amplification of the tkt gene -

PS Example 6; Page 43-46; 53pp; English.

XX
CC The invention relates to the preparation of L-amino acids comprising
CC fermenting L-amino acid-producing coryneform bacteria which
CC overexpresses a gene e.g. that for transketolase, tkt. Also
CC included are transformed coryneform microorganisms harbouring the
CC plasmid pC-118mb2 which contains the tkt gene. The method is useful for
CC the fermentative preparation of L-amino acids, i.e. L-lysine, L-threonine
CC and L-isoleucine, in which at least the tkt gene is amplified. L-lysine,
CC L-threonine and L-isoleucine are useful in animal nutrition, in human
CC medicine and in the pharmaceuticals industry. The present sequence
CC is the gene for pyruvate oxidase, poxh, which was eliminated by mutation
CC in a strain expressing with tkt in order to further increase yields of
CC L-amino acids.

XX Sequence 2160 BP; 491 A; 486 C; 647 G; 536 T; 0 other;

Query Match 100.0%; Score 2160; DB 22; Length 2160;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGAGGCGATCTGTGAGTGCATCTTTTGGGGGCGGCTAAATTTGGCCACTTT 60
DB 1 TTAGAGGCGATCTGTGAGTGCATCTTTTGGGGGCGGCTAAATTTGGCCACTTT 60
QY 61 CGAGCGACCAACAGAGCGGTGCCAGATGTTTAAATAGCGATGCGGCGATCTGT 120
DB 61 CGAGCGACCAACAGAGCGGTGCCAGATGTTTAAATAGCGATGCGGCGATCTGT 120
QY 121 TTGGTTTGACGGGTGAACCAACAGACTGCCACAGACGAGAAATCCCAAAAGT 180
DB 121 TTGGTTTGACGGGTGAACCAACAGACTGCCACAGACGAGAAATCCCAAAAGT 180
QY 181 GGGCATCCCTGTTTGGTACCGAGTACCCAGCCGCGCTGAAATCCTCTGGCAGCGGGG 240
DB 181 GGGCATCCCTGTTTGGTACCGAGTACCCAGCCGCGCTGAAATCCTCTGGCAGCGGGG 240
QY 241 AAGCGTGGCAACACTGGAATTTAAGACACAAATTTGAAGTGGCACCAAGTTAGCCACAC 300
DB 241 AAGCGTGGCAACACTGGAATTTAAGACACAAATTTGAAGTGGCACCAAGTTAGCCACAC 300
QY 301 AATAGCCATACGTTGAGAGTTCAGATGACACAGCTACGCAAGAAATTAATTGACA 360
DB 301 AATAGCCATACGTTGAGAGTTCAGATGACACAGCTACGCAAGAAATTAATTGACA 360
QY 361 CTTTGGAAAGCTCAAGGTGTGAAGCGAATTTATGTTGGTGGTGACACCTTAATCCGA 420
DB 361 CTTTGGAAAGCTCAAGGTGTGAAGCGAATTTATGTTGGTGGTGACACCTTAATCCGA 420
QY 421 TCGNGAGTCTGTCCCGCAATCATATATTGAGTGGGTGCAAGCTTGAAATAGAGAGCGG 480
DB 421 TCGNGAGTCTGTCCCGCAATCATATATTGAGTGGGTGCAAGCTTGAAATAGAGAGCGG 480
QY 481 CGGGGTTTGACGCGGTGCGGAATCGTTGATCAGTGGGGAGCTGGGAGTATGCTGCTT 540
DB 481 CGGGGTTTGACGCGGTGCGGAATCGTTGATCAGTGGGGAGCTGGGAGTATGCTGCTT 540
QY 541 CTTGTGCTCTGGAACACACACTGATTCAGGGCTTTATGATTCGATCGAAATGGTG 600
DB 541 CTTGTGCTCTGGAACACACACTGATTCAGGGCTTTATGATTCGATCGAAATGGTG 600
QY 601 CGAAGGTGTGGCATGCTAGCATATTCGAGTGGCCAGATTTGGTTCGAGTCTTCC 660

DB 601 CGAAGGTGTGGCATGCTAGCATATTCGAGTGGCCAGATTTGGTTCGAGTCTTCC 660
QY 661 AGGAACGATCCGGAATTTTGTAAAGAAATGCTGTGTTACTGAGATGTAATG 720
DB 661 AGGAACGATCCGGAATTTTGTAAAGAAATGCTGTGTTACTGAGATGTAATG 720
QY 721 GTGTGAGACAGGTGAAACGATTTGATCAGCGATTCAGTCCACCATGCGGTAAG 780
DB 721 GTGTGAGACAGGTGAAACGATTTGATCAGCGATTCAGTCCACCATGCGGTAAG 780
QY 781 GTGTGAGACAGGTGAAACGATTTGATCAGCGATTCAGTCCACCATGCGGTAAG 840
DB 781 GTGTGAGACAGGTGAAACGATTTGATCAGCGATTCAGTCCACCATGCGGTAAG 840
QY 841 ATTCCATTTCCACTATTTTCTTGGCACTCTGTGTTTCCGGAATCCACTAGAGCTG 900
DB 841 ATTCCATTTCCACTATTTTCTTGGCACTCTGTGTTTCCGGAATCCACTAGAGCTG 900
QY 901 CAGCGCTGTGAGCGGATTAACACAGCTAAGTCTGCACTTGTCTGCGGTGCGGCG 960
DB 901 CAGCGCTGTGAGCGGATTAACACAGCTAAGTCTGCACTTGTCTGCGGTGCGGCG 960
QY 961 TGAAGATGCTCGCGCGAGGTGTGAGATTTGGCGGAGAAAGATTAAATCACCATCGGC 1020
DB 961 TGAAGATGCTCGCGCGAGGTGTGAGATTTGGCGGAGAAAGATTAAATCACCATCGGC 1020
QY 1021 ATGCGCTGGTGTAAAGAGTACATCCAGATGAGAAATCGTTTGGTGGAGATCTTG 1080
DB 1021 ATGCGCTGGTGTAAAGAGTACATCCAGATGAGAAATCGTTTGGTGGAGATCTTG 1080
QY 1081 GCCTGCTGTGTTACGCGCGCTGCTGAGATGCGTCCAAATAGCGCGATGCTGATCTAT 1140
DB 1081 GCCTGCTGTGTTACGCGCGCTGCTGAGATGCGTCCAAATAGCGCGATGCTGATCTAT 1140
QY 1141 TGGGTAAGGATTTCCCTTATTCGATTTCCCTCTAAACAGAAAGTGGCCAGGTGATA 1200
DB 1141 TGGGTAAGGATTTCCCTTATTCGATTTCCCTCTAAACAGAAAGTGGCCAGGTGATA 1200
QY 1201 TCAACGTTGCGCACATTTGGTTCAGCTTACACAGGTGAAGTATCCGGTACCGGTGATGTTG 1260
DB 1201 TCAACGTTGCGCACATTTGGTTCAGCTTACACAGGTGAAGTATCCGGTACCGGTGATGTTG 1260
QY 1261 CTGCAACAATCGAAATATTTTGGCTCATGTGAAGAAAAACAGATGCTTCTCTTG 1320
DB 1261 CTGCAACAATCGAAATATTTTGGCTCATGTGAAGAAAAACAGATGCTTCTCTTG 1320
QY 1321 ATCGATGCTCAAGGACACAGCGATTAAGTGAAGTGGTGGTGAAGAGATGACACATA 1380
DB 1321 ATCGATGCTCAAGGACACAGCGATTAAGTGAAGTGGTGGTGAAGAGATGACACATA 1380
QY 1381 ACGTGAAGAGCATGTGCTTATTCACCTGATAGCTTGCCTATTTTGAAGAGAGCTGG 1440
DB 1381 ACGTGAAGAGCATGTGCTTATTCACCTGATAGCTTGCCTATTTTGAAGAGAGCTGG 1440
QY 1441 CGGATTAAGATGCGGTGTTTACTGTGAGTACCGGATGTCATGTGTGCGATGCGAGGT 1500
DB 1441 CGGATTAAGATGCGGTGTTTACTGTGAGTACCGGATGTCATGTGTGCGATGCGAGGT 1500
QY 1501 ACATGAGAAATCCGAGGAAACGCGGCACTTGTGGTTCATTCGCCACGCGACAGATG 1560
DB 1501 ACATGAGAAATCCGAGGAAACGCGGCACTTGTGGTTCATTCGCCACGCGACAGATG 1560
QY 1561 CTAATGCGTGTGCTCATGCTGATGCTGCGCAAAAGTGTGATGAAACCGCCAGGTATG 1620
DB 1561 CTAATGCGTGTGCTCATGCTGATGCTGCGCAAAAGTGTGATGAAACCGCCAGGTATG 1620
QY 1621 CGATGTGAGGAGTGTGTTGGGATGCTGCTGGTGAAGTGTGACCGTTAAGCTGC 1680
DB 1621 CGATGTGAGGAGTGTGTTGGGATGCTGCTGGTGAAGTGTGACCGTTAAGCTGC 1680
QY 1681 ACGAATTCGCTGAGGCTGTGTTTAAACACAGTCTTGGGCAATGGTGAAGTGG 1740
DB 1681 ACGAATTCGCTGAGGCTGTGTTTAAACACAGTCTTGGGCAATGGTGAAGTGG 1740

Db	1661	ACCAACTTCGCGCTAAGAGGCTGTGGTGTGTTTAAACAACAGTTCCTTTGGGCATGCTGAAGTTGG	1740
QY	1741	AGATGCTCTGTGGAGGACACGCCAGAAATTTGGTACTGACCATGAGAGAGTGAATTTCCAG	1800
Db	1741	AGATGCTCTGTGGAGGACACGCCAGAAATTTGGTACTGACCATGAGAGAGTGAATTTCCAG	1800
QY	1801	AGATTGGGGCGCGTGGCGGATCAAAATCGTACGATCACCAGATCCGAGAAAGTTGCGG	1860
Db	1801	AGATTGGGGCGCGTGGCGGATCAAAATCGTACGATCACCAGATCCGAGAAAGTTGCGG	1860
QY	1861	AGCAGCTAGCTGAGGAGCATTTGGCATATTCCTGGACCTGTACTGATGATATGCTACGGATC	1920
Db	1861	AGCAGCTAGCTGAGGAGCATTTGGCATATTCCTGGACCTGTACTGATGATATGCTACGGATC	1920
QY	1921	CTATGGCGTGTTCATCCCAACCACTCACGTGGGAACAAGTATGGATTCAGCAAG	1980
Db	1921	CTATGGCGTGTTCATCCCAACCACTCACGTGGGAACAAGTATGGATTCAGCAAG	1980
QY	1981	CGGCGACCCGCAACCGTCTTGTGTGGAGAGTAGAGAGGATGATGATCTGGCCCGTTCGA	2040
Db	1981	CGGCGACCCGCAACCGTCTTGTGTGGAGAGTAGAGAGGATGATGATCTGGCCCGTTCGA	2040
QY	2041	ACATAGGAAATATTTCTTACTTCATGATGATTTGATATACACGTGCTGTTCTCATTTGACCCGA	2100
Db	2041	ACATAGGAAATATTTCTTACTTCATGATGATTTGATATATACACGTGCTGTTCTCATTTGACCCGA	2100
QY	2101	GGCGTTAACTGCCCAACATTTCCAGAGATGGAGCAAGCGCGGGTCCCATGAGAAATGGCCT	2160
Db	2101	GGCGTTAACTGCCCAACATTTCCAGAGATGGAGCAAGCGCGGGTCCCATGAGAAATGGCCT	2160

RESULT 2

ID	AAD20203	AAD20203 standard; DNA; 2160 BP.
XX	AAD20203;	
XX	03-JAN-2002 (first entry)	
XX	Corynebacterium glutamicum pyruvate oxidase (poxb) DNA.	
XX	L-amino acid; fermentation; coryneform bacteria; animal nutrition; glucose 6-phosphate dehydrogenase; zwf; human medicine; foodstuff industry; pyruvate oxidase; poxb; pharmaceutical industry; ds.	
XX	Corynebacterium glutamicum.	
XX	Key	Location/Qualifiers
XX	CDS	327..2066
XX	FT	/*tag= a
XX	FT	/product= "Pyruvate oxidase (poxb) "
XX	WT	WO200170995-A1.
XX	27-SEP-2001.	
XX	05-JUL-2000; 2000WO-EP06303.	
XX	20-MAR-2000; 2000US-0531269.	
XX	(DEGS) DEGUSA AG.	
XX	(KERJ) FORSCHUNGSZENTRUM JUELICH GMBH.	
XX	(UYNA-) UNIV NAT IRELAND.	
XX	Burke K, Sahn H, Eggeling L, Moritz B, Dunlcan LK, McCormack A; Stapleton C, Moeckel B, Thierbach G;	
XX	WPI; 2001-639130/73.	
XX	P-PSDB; AAE12462.	
XX	Preparing L-amino acids by fermenting coryneform bacteria transformed with the glucose 6-phosphate dehydrogenase gene is particularly useful	

Query Match	Best Local Similarity	100.0%	Score 2160;	DB 22;	Length 2160;
Matches 2160;	Conservative	0;	Mismatches	0;	Indels
					Gaps
1	TTAGAGGCGATTCCTGTGAGCGTCACTTTTGGGGGTCGGGGCTAAATTTGGCCAGTTT				60
1	TTAGAGGCGATTCCTGTGAGCGTCACTTTTGGGGGTCGGGGCTAAATTTGGCCAGTTT				60
61	CGAGGCGACACAGACAGGCGTCCACGATGTTTAAATAGGCGATCGTGCGCATCTGT				120
61	CGAGGCGACACAGACAGGCGTCCACGATGTTTAAATAGGCGATCGTGCGCATCTGT				120
121	TTGGTTTCGAGGCGGTGGAACCAACCCAGACTGCCACCAACGACGGAATCCCAAACT				180
121	TTGGTTTCGAGGCGGTGGAACCAACCCAGACTGCCACCAACGACGGAATCCCAAACT				180
181	GGGATCCCTTTTGGTACCGAGTACCCACCCGGGCTGAAATCCCTGGGACGGGCGG				240
181	GGGATCCCTTTTGGTACCGAGTACCCACCCGGGCTGAAATCCCTGGGACGGGCGG				240
241	AAGCGTGGCAACAACCTGGAATTTAAGACACAAATTTAAGTGGACCAAGTTAGGCAAC				300
241	AAGCGTGGCAACAACCTGGAATTTAAGACACAAATTTAAGTGGACCAAGTTAGGCAAC				300
301	AATAGCCATACAGTTTGAGAGCTTACATGACACACAGCTACGACAGACAAATTAATGACA				360
301	AATAGCCATACAGTTTGAGAGCTTACATGACACACAGCTACGACAGACAAATTAATGACA				360
361	CTTTGGAAGCTCAAGAGGTGTAAGGAATTTATGGTTGGTGGGACGCTTATCCGA				420
361	CTTTGGAAGCTCAAGAGGTGTAAGGAATTTATGGTTGGTGGGACGCTTATCCGA				420
421	TCGTGATGCTGTCCGCCAATCAGATATTGAGTGGGTGACAGTTTGAATAGGAAGCG				480
421	TCGTGATGCTGTCCGCCAATCAGATATTGAGTGGGTGACAGTTTGAATAGGAAGCG				480
481	CGGCGTTTGACACCGCGGTGCGGAATCGTTGATCACTGGGAGCTGACGATGTGCTCTT				540
481	CGGCGTTTGACACCGCGGTGCGGAATCGTTGATCACTGGGAGCTGACGATGTGCTCTT				540
541	CTTGTGTCTCGGAACACACACACTGATTCAGGCTCTTATGATTCGATCGAATGGTG				600
541	CTTGTGTCTCGGAACACACACACTGATTCAGGCTCTTATGATTCGATCGAATGGTG				600
601	CGAAGGTGTTGCCATCGCTAGCCATATTCGAGTGGCCAGATTTGTTTGCAGTCTTCC				660
601	CGAAGGTGTTGCCATCGCTAGCCATATTCGAGTGGCCAGATTTGTTTGCAGTCTTCC				660
661	AGGAAGCGCATCCGGAATTTTGTAAAGAAATGCTCTGTGTTACTGGAGATGTGATG				720
661	AGGAAGCGCATCCGGAATTTTGTAAAGAAATGCTCTGTGTTACTGGAGATGTGATG				720
721	GTGTGTGAGCGAGGTGGAAGCAATTTTGATACCGGATTCAGTCCACCATGGCGGTAAG				780
721	GTGTGTGAGCGAGGTGGAAGCAATTTTGATACCGGATTCAGTCCACCATGGCGGTAAG				780
781	GTGTGTGAGCGAGGTGGAAGCAATTTTGATACCGGATTCAGTCCACCATGGCGGTAAG				840
781	GTGTGTGAGCGAGGTGGAAGCAATTTTGATACCGGATTCAGTCCACCATGGCGGTAAG				840

Dp	781	GTGTGTGGTGGTGGTGGTATCTCGTGTGATATCGCTAAGGAAGACGCAGAGTACGGTACT	840
Qy	841	ATTCCAAATTCCACATATTCTTCTTGGGACCTCTGCGGTGTCCCGGATCCTACTAGCTG	900
Dp	841	ATTCCAAATTCCACATATTCTTCTTGGCACTCTGCGGTGTCCCGGATCCTACTAGCTG	900
Qy	901	CAGCGCTGTGGAGGCGATTAAACAAACCTAAGTGTGCACCTTGTCTGCGGTGCGGGCG	960
Dp	901	CAGCGCTGTGGAGGCGATTAAACAAACCTAAGTGTGCACCTTGTCTGCGGTGCGGGCG	960
Qy	961	TGAAGAAATGCTCGCGCGAGGTGTGAGATTGCGGAGAAAGATTAAATCACCGATCGGGC	1020
Dp	961	TGAAGAAATGCTCGCGCGAGGTGTGAGATTGCGGAGAAAGATTAAATCACCGATCGGGC	1020
Qy	1021	ATGCGCGTGGGTGGTGAACAGTACACTGCAGATGAGATTCGGTTGAGGTGGCGATGCTG	1080
Dp	1021	ATGCGCGTGGGTGGTGAACAGTACACTGCAGATGAGATTCGGTTGAGGTGGCGATGCTG	1080
Qy	1081	GCTGTCTTGGTTACGGCGCCTGCGGTGATGCGTCAATGAGCGGATCTGCTGATTCAT	1140
Dp	1081	GCTGTCTTGGTTACGGCGCCTGCGGTGATGCGTCAATGAGCGGATCTGCTGATTCAT	1140
Qy	1141	TGGGTACGGATTTCCCTATTCTTCATTTTCCCTCTTAAAGAACAGTTGCCAGGTGATA	1200
Dp	1141	TGGGTACGGATTTCCCTATTCTTCATTTTCCCTCTTAAAGAACAGTTGCCAGGTGATA	1200
Qy	1201	TCAACGGTGTGGACATTGTGTGACGTACCAAGGTGAAGTATCCGCTGACCGGTATGTTG	1260
Dp	1201	TCAACGGTGTGGACATTGTGTGACGTACCAAGGTGAAGTATCCGCTGACCGGTATGTTG	1260
Qy	1261	CTGCACAAATCGAAAATATTTTGGCTCATGTGAAGGAAAAACAGATCTTCTTCTTGTG	1320
Dp	1261	CTGCACAAATCGAAAATATTTTGGCTCATGTGAAGGAAAAACAGATCTTCTTCTTGTG	1320
Qy	1321	ATCGATGTCTCAAGGCGACAGAGGCTGAAGTGAAGCTGGGTGTGAGAGCGTACACACTA	1380
Dp	1321	ATCGATGTCTCAAGGCGACAGAGGCTGAAGTGAAGCTGGGTGTGAGAGCGTACACACTA	1380
Qy	1381	ACGTGGAAGACATGTGTCTATTTCACCTCGTAATACGTTGCTCTATTTTGAACGAGCTGG	1440
Dp	1381	ACGTGGAAGACATGTGTCTATTTCACCTCGTAATACGTTGCTCTATTTTGAACGAGCTGG	1440
Qy	1441	CGGATTAAGGATGCGGTGTCTTACTGTGATACCGGCAATGTGCAATGTGGGATCGAGGT	1500
Dp	1441	CGGATTAAGGATGCGGTGTCTTACTGTGATACCGGCAATGTGCAATGTGGGATCGAGGT	1500
Qy	1501	ACATCGAAGATCCGAGAGGAAACGCGCGCATTTGTGGGTTCATTCGCGCACGCGACGATGG	1560
Dp	1501	ACATCGAAGATCCGAGAGGAAACGCGCGCATTTGTGGGTTCATTCGCGCACGCGACGATGG	1560
Qy	1561	CTAATGCGTTCCTCATATCCATTTGGTGTGGGAAATGTTGATCGAAACCGCCAGGTGATCG	1620
Dp	1561	CTAATGCGTTCCTCATATCCATTTGGTGTGGGAAATGTTGATCGAAACCGCCAGGTGATCG	1620
Qy	1621	CGATGTGTGGCGATGTGTGTTGGGCAATGCTGTGCGGTGACCTTCTGACCTTAAAGCTGC	1680
Dp	1621	CGATGTGTGGCGATGTGTGTTGGGCAATGCTGTGCGGTGACCTTCTGACCTTAAAGCTGC	1680
Qy	1681	ACCAACTTCCGCTAAGGCTGTGGTGTAAACAACAGTTCTTGTGGGCACTGTGTGAAGTTGG	1740
Dp	1681	ACCAACTTCCGCTAAGGCTGTGGTGTAAACAACAGTTCTTGTGGGCACTGTGTGAAGTTGG	1740
Qy	1741	AGATGTCTGTGGAGGAGACGCCAAGATTTGGTACTGACCATGAGGAAATGTGAATTTCCGAG	1800
Dp	1741	AGATGTCTGTGGAGGAGACGCCAAGATTTGGTACTGACCATGAGGAAATGTGAATTTCCGAG	1800
Qy	1801	AGATTGGCGGCTGCGGATCAAAATCGTACGCATCCGATCCGAAAGAAAGTTTCGCG	1860
Dp	1801	AGATTGGCGGCTGCGGATCAAAATCGTACGCATCCGATCCGAAAGAAAGTTTCGCG	1860
Qy	1861	AGCAGCTAAGCTAGAGGCAATGGCAATCTCGGACCTGTATCTGATGATATGTCTACGATCTC	1920
Dp	1861	AGCAGCTAAGCTAGAGGCAATGGCAATCTCGGACCTGTATCTGATGATATGTCTACGATCTC	1920

OY		1921	CTATGGGCGTGTGCATCCCAACCAACCATTCACGTGGAAAGGTCATGSGAATTTCAGCAAG	1980			
Db		1921	CTATGGGCGTGTGCATCCCAACCAACCATTCACGTGGAAAGGTCATGSGAATTTCAGCAAG	1980			
OY		1981	CGGCCACCAGCAGCGTTTGCTGGTAGAGAGTAGAGGAGATGATCTGGCCCCGTTGCA	2040			
Db		1981	CGGCCACCAGCAGCGTTTGCTGGTAGAGAGTAGAGGAGATGATCTGGCCCCGTTGCA	2040			
OY		2041	ACATAAGGAATATTCCTACATCCATGATGATGATGATACACCTGCTTCCTATTGACCGCA	2100			
Db		2041	ACATAAGGAATATTCCTACATCCATGATGATGATGATACACCTGCTTCCTATTGACCGCA	2100			
OY		2101	GCGCTTAAGTCCCAACAATTTCCAGAGATGGCAGCTCACGCCGCGTCCCAGATGAGATTGCCCT	2160			
Db		2101	GCGCTTAAGTCCCAACAATTTCCAGAGATGGCAGCTCACGCCGCGTCCCAGATGAGATTGCCCT	2160			
<hr/>							
RESULT 3							
ID	AAI65506	AAI65506 standard; DNA; 2160 BP.					
XX	AAI65506:						
DT	10-DEC-2001	(first entry)					
DE	Nucleotide sequence of the Corynebacterium poxb gene.						
XX							
KW	gnd gene; 6-phosphogluconate dehydrogenase; L-amino acid; L-lysine;						
XX	L-threonine; L-tryptophan; poxb gene; pyruvate oxidase; ss.						
OS	Corynebacterium glutamicum.						
XX							
FH	Key	Location/Qualifiers					
FT	CDS	327..2066					
FT		/*tag-a					
FT		/product- "pyruvate oxidase"					
PN	WO200171012-A1.						
XX							
PD	27-SEP-2001.						
XX							
PE	05-JUL-2000; 2000WO-EPO6299.						
XX							
PR	20-MAR-2000; 2000US-0531265.						
XX							
PA	(DEGS) DEGUSSA AG.						
PA	(DYNAL-) DYNIV NAT IRELAND.						
PI	Dunitau LR, McCormack A, Stapelton C, Burke K, Moeckel B;						
DR	WPI; 2001-602792/68.						
DR	P-PSTDB: AAG79096.						
PT							
PT	Preparing L-amino acids by fermenting coryneform bacteria transformed						
PT	with the 6-phosphogluconate dehydrogenase gene is particularly useful						
PT	to produce L-lysine and L-threonine -						
PS	Example 9; Page 47-50; 59pp; English.						
XX							
CC	The present sequence represents the poxb gene of Corynebacterium						
CC	glutamicum. The poxb gene encodes a pyruvate oxidase enzyme. The						
CC	poxb gene and the gnd gene are used to produce recombinant bacteria						
CC	for use in the course of the invention. The gnd gene encodes a						
CC	6-phosphogluconate dehydrogenase enzyme. The specification describes						
CC	a method for the fermentative preparation of L-amino acids, in						
CC	particular L-lysine, L-threonine, and L-tryptophan. The method comprises						
CC	fermenting coryneform bacteria in which at least the gnd gene is						
CC	amplified and overexpressed. The L-amino acids produced are used in						
CC	animal nutrition, human medicine and the pharmaceuticals industry.						
SQ	Sequence 2160 BP; 491 A; 486 C; 647 G; 536 T; 0 other.						

Query Match		100.0%	Score 2160:	DB 22:	Length 2160:
Best Local Similarity 100.0%:		Pred. No. 0:			
Matches 2160:		Conservative 0:	Mismatches 0:	Indels 0:	Gaps 0:
QY	1	TTAGAGCGATTTCTGTAGAGTCACTTTTGTGGGGTGGGGTCTAAATTTGGCCAGTTT	60		
DB	1	TTAGAGCGATTTCTGTAGAGTCACTTTTGTGGGGTGGGGTCTAAATTTGGCCAGTTT	60		
QY	61	CGAGGCGACGAGAGGCGTCCACGATGTTAAATAGGAGATGGGGATCTGTG	120		
DB	61	CGAGGCGACGAGAGGCGTCCACGATGTTAAATAGGAGATGGGGATCTGTG	120		
QY	121	TTGTTTTCGAGGGGCTGAACCAACAGACTGGCCAGCAACGAGCAAAATCCCAAAAGT	180		
DB	121	TTGTTTTCGAGGGGCTGAACCAACAGACTGGCCAGCAACGAGCAAAATCCCAAAAGT	180		
QY	181	GGGATCCCTTTTGGTACCGAGTACCCACCGGGGCTGAACACTCCCTGGAGGGGGG	240		
DB	181	GGGATCCCTTTTGGTACCGAGTACCCACCGGGGCTGAACACTCCCTGGAGGGGGG	240		
QY	241	AAGCGTGGCAACACTGGATTTAAGACACATTTAAGTCCGACCAAGTTAGGCAACAC	300		
DB	241	AAGCGTGGCAACACTGGATTTAAGACACATTTAAGTCCGACCAAGTTAGGCAACAC	300		
QY	301	AATAGCCATTAACGTTGAGAGATTAGATGGCAGACAGTACGAGCAATTAATTGACA	360		
DB	301	AATAGCCATTAACGTTGAGAGATTAGATGGCAGACAGTACGAGCAATTAATTGACA	360		
QY	361	CTTTGGAAGCTCAAGGTGTGAAGCAATTTATGGTTTGGTGGTGGAGACGCTTATCCGA	420		
DB	361	CTTTGGAAGCTCAAGGTGTGAAGCAATTTATGGTTTGGTGGTGGAGACGCTTATCCGA	420		
QY	421	TGCTGATGCTGTCCGCCAATCAGATATTGAGTGGGTGCACGTTTGAATGAGCAAGCGG	480		
DB	421	TGCTGATGCTGTCCGCCAATCAGATATTGAGTGGGTGCACGTTTGAATGAGCAAGCGG	480		
QY	481	CGGCTTTGACAGCGGTGGGATCGTGTATCAGTGGGGAGCTGGCAGTATGCTGCTT	540		
DB	481	CGGCTTTGACAGCGGTGGGATCGTGTATCAGTGGGGAGCTGGCAGTATGCTGCTT	540		
QY	541	CTTGTGTCTGGAAACACACACTGATTCAGGGTCTTTATGATTCGCATCGAAATGCTG	600		
DB	541	CTTGTGTCTGGAAACACACACTGATTCAGGGTCTTTATGATTCGCATCGAAATGCTG	600		
QY	601	CGAAGGTGTGGGCTTCGCTAGCCATATTCGAGTGGCCAGATGGTTCGACGTTTCC	660		
DB	601	CGAAGGTGTGGGCTTCGCTAGCCATATTCGAGTGGCCAGATGGTTCGACGTTTCC	660		
QY	661	AGCAAGCATCCGAGATTTTGTAAAGAAATGCTGTGTTACTGCGAGATGGGAATG	720		
DB	661	AGCAAGCATCCGAGATTTTGTAAAGAAATGCTGTGTTACTGCGAGATGGGAATG	720		
QY	721	GTTGGTGGAGAGGTTAAGCATTTTGCATCAGCGATTCAGTCCACATGGGGGTAAAG	780		
DB	721	GTTGGTGGAGAGGTTAAGCATTTTGCATCAGCGATTCAGTCCACATGGGGGTAAAG	780		
QY	781	GTTGTGCGTGTAGTATCTGCTGTATATCGCTAAGGAGAGCAGAGATGACGTTACTT	840		
DB	781	GTTGTGCGTGTAGTATCTGCTGTATATCGCTAAGGAGAGCAGAGATGACGTTACTT	840		
QY	841	AFTCCAAATTCACATTTCTTCTGTGCACTCCTGTGTGCTCCGATCTTACTGAGGCTG	900		
DB	841	AFTCCAAATTCACATTTCTTCTGTGCACTCCTGTGTGCTCCGATCTTACTGAGGCTG	900		
QY	901	CAGCGCTGTGAGAGCGATTAACAACGCTAAGTCTGATCTTGTGCGGGTGGGGCG	960		
DB	901	CAGCGCTGTGAGAGCGATTAACAACGCTAAGTCTGATCTTGTGCGGGTGGGGCG	960		
QY	961	TGAGAAATGCTGCGCGCAGAGTGTGAGTGGCGAGAAATTAATTAACCGATCGGCG	1020		
DB	961	TGAGAAATGCTGCGCGCAGAGTGTGAGTGGCGAGAAATTAATTAACCGATCGGCG	1020		
QY	1021	ATGCGCTGGTGTGTAAGCATACATCCAGCATGAGAAATCCGTTGAGGTCCGATGTCTG	1080		
DB	1021	ATGCGCTGGTGTGTAAGCATACATCCAGCATGAGAAATCCGTTGAGGTCCGATGTCTG	1080		
QY	1081	GCCTGCTGTGTTACGGGCGCTGCTGTGATGCGTCCATATAGGGGATCTGTGATTTCTAT	1140		
DB	1081	GCCTGCTGTGTTACGGGCGCTGCTGTGATGCGTCCATATAGGGGATCTGTGATTTCTAT	1140		
QY	1141	TGGTACGAGATTTCCCTTATTCGATTTCTTCTTAAAGCAACAGTTGGCCAGGTGATA	1200		
DB	1141	TGGTACGAGATTTCCCTTATTCGATTTCTTCTTAAAGCAACAGTTGGCCAGGTGATA	1200		
QY	1201	TCAACGGTGGCAATTTGTTGTCAGTACACGAGTGAAGTATCCGTTAGCCGTGATGTTG	1260		
DB	1201	TCAACGGTGGCAATTTGTTGTTGTCAGTACACGAGTGAAGTATCCGTTAGCCGTGATGTTG	1260		
QY	1261	CTGCACAAATCAGAAATATTTTCCCTCATATGTAAGGAAAAACAGATCGTCTCTCCG	1320		
DB	1261	CTGCACAAATCAGAAATATTTTCCCTCATATGTAAGGAAAAACAGATCGTCTCTCCG	1320		
QY	1321	ATCGATGCTCAAGGCAACAGAGCTAAGTTAGCTCGGTGTAGAGACGTACACAAAT	1380		
DB	1321	ATCGATGCTCAAGGCAACAGAGCTAAGTTAGCTCGGTGTAGAGACGTACACAAAT	1380		
QY	1381	ACGTCGAGAGCATGTCCTATTCACCCCTGAATACGTTGCTTATTTGAAGAGCTGG	1440		
DB	1381	ACGTCGAGAGCATGTCCTATTCACCCCTGAATACGTTGCTTATTTGAAGAGCTGG	1440		
QY	1441	CGGATTAAGATGCGGTTTACTGTGATACCGGCAATGTCAAATGTGTGGCATGCGAGT	1500		
DB	1441	CGGATTAAGATGCGGTTTACTGTGATACCGGCAATGTCAAATGTGTGGCATGCGAGT	1500		
QY	1501	ACATCGAATTCGCGAGAGAACCGGCACTTGTGGTTCATTTCCGACAGGCAAGTGG	1560		
DB	1501	ACATCGAATTCGCGAGAGAACCGGCACTTGTGGTTCATTTCCGACAGGCAAGTGG	1560		
QY	1561	CTAATGCGTCCCTCATGCGATTTGGTGGCGAAAGTGTGTCGAAACCGCAGATGATCG	1620		
DB	1561	CTAATGCGTCCCTCATGCGATTTGGTGGCGAAAGTGTGTCGAAACCGCAGATGATCG	1620		
QY	1621	CGATGTGTGCGATGTTGTTGGGCTGCTGGGTGAGCTTGTGACCGTTAAGCTGC	1680		
DB	1621	CGATGTGTGCGATGTTGTTGGGCTGCTGGGTGAGCTTGTGACCGTTAAGCTGC	1680		
QY	1681	ACCACCTTCGCGGAAGAGCTGTGTGTTTAAACAAGTCTTTGGGATGTAAGTGG	1740		
DB	1681	ACCACCTTCGCGGAAGAGCTGTGTGTTTAAACAAGTCTTTGGGATGTAAGTGG	1740		
QY	1741	AGATGCTGTGGAAGGACAGCCAGAAATTTGTAAGTCCATGAGAGAAATGATTTGCGAG	1800		
DB	1741	AGATGCTGTGGAAGGACAGCCAGAAATTTGTAAGTCCATGAGAGAAATGATTTGCGAG	1800		
QY	1801	AGATTGGGGGCGTGGCGGTATCAAAATCGGTATCGATCAGCGATCCGAAAGATTCGCG	1860		
DB	1801	AGATTGGGGGCGTGGCGGTATCAAAATCGGTATCGATCAGCGATCCGAAAGATTCGCG	1860		
QY	1861	AGCAGTAGCTGAGAGCATTTGGCATATCTTGACCTGTACTGATGATATGTCACGATC	1920		
DB	1861	AGCAGTAGCTGAGAGCATTTGGCATATCTTGACCTGTACTGATGATATGTCACGATC	1920		
QY	1921	CTAATGCGTGTGATCCACCAACATTCACGTTGGGAGAGGTCATGGGATTCAGCAGG	1980		
DB	1921	CTAATGCGTGTGATCCACCAACATTCACGTTGGGAGAGGTCATGGGATTCAGCAGG	1980		
QY	1981	CGGCGACCGCAACGCTTTTGGTGGAGAGTATGAGAGATGATCGATCTGGCGGTTCGA	2040		
DB	1981	CGGCGACCGCAACGCTTTTGGTGGAGAGTATGAGAGATGATCGATCTGGCGGTTCGA	2040		
QY	2041	ACATTAAGAAATATTTCTACTCATGATGATTTATACACTGCTGTCTCATTTGACCGCGA	2100		
DB	2041	ACATTAAGAAATATTTCTACTCATGATGATTTATACACTGCTGTCTCATTTGACCGCGA	2100		
QY	2101	GGCGTTAAGTCCCAACTTTCCAGATGGAGCTCAAGCGGAGCCATGATGATGGCTT	2160		
DB	2101	GGCGTTAAGTCCCAACTTTCCAGATGGAGCTCAAGCGGAGCCATGATGATGGCTT	2160		

Db 2101 GCGCTTAACGCCACATTTCAGAGATGCGAGCTACGCCGGTGCCCATGAGATTGCCCT 2160

RESULT 4
AA61779
ID AAF61779 standard; DNA; 2160 BP.
XX
AC AAF61779;
XX
DT 27-JUL-2001 (first entry)
XX
DE C. glutamicum ATCC13032 poxb DNA.
XX
KW Pyruvate oxidase; poxb; E.C. 1.2.2.2; mutagenesis; coryneform bacteria;
KW fermentation; L-amino acid production; L-lysine production; medicine;
KW food production; animal nutrition; ds.
XX
OS Corynebacterium glutamicum.
XX
FH Key Location/Qualifiers
FT -35_signal 227..232
FT /*tag- a
FT /note- "As given in the specification"
FT -10_signal 256..261
FT /*tag- b
FT /note- "As given in the specification"
FT CDS 327..2066
FT /*tag- c
FT /product- "poxb"
XX
PN EP1096013-A2.
XX
PD 02-MAY-2001.
XX
PF 14-OCT-2000; 2000EP-0122505.
XX
PR 28-OCT-1999; 99DE-1051975.
XX
PA (DEGS) DEGUSA AG.
XX
PI Moeckel B, Weissenborn A, Pfeifferle W, Fuehler A, Kalinowski J;
PI Bathe B, Dusch N;
XX
DR WPI: 2001-309855/33.
DR P-PDB: AAB70908.
XX
PT New Coryneform glutamicum poxb pyruvate oxidase polynucleotide useful
PT for insertional mutation, producing strains with increased production
PT of amino acids
XX
PS Claim 4; Page 13-16; 21pp; German.
XX
CC This invention describes a novel polynucleotide (I) which is used for
CC insertional mutagenesis of the poxb gene in coryneform bacteria. The poxb
CC gene can be used for fermentative production of L-amino acids,
CC specifically L-lysine, which is used in human medicine, foods and
CC especially animal nutrition. (I) is also useful as a source of probes and
CC primers for isolation of related sequences. Cells in which the poxb gene
CC is suppressed produce higher yields of L-amino acids. This sequence
CC encodes the pyruvate oxidase (E.C. 1.2.2.2) poxb gene from
CC Corynebacterium glutamicum ATCC13032 which is described in the invention.
XX
SQ Sequence 2160 BP; 491 A; 486 C; 647 G; 536 T; 0 other;

Query Match 100.0%; Score 2160; DB 22; Length 2160;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGAGGCGATTCTGAGGCTACTTTTGTGGGCTGGGCTTAATTGGCCACTTT 60
DB 1 TTAGAGGCGATTCTGAGGCTACTTTTGTGGGCTGGGCTTAATTGGCCACTTT 60
QY 61 CGAGGCGACGACGAGCGGTGCCACGATGTTTAATAGCGATCGGTGGCGATCTGTGT 120

Db 61 CGAGGCGACGACGAGCGGTGCCACGATGTTTAATAGCGATCGGTGGCGATCTGTGT 120
QY 121 TTGCTTGCAGGGCTGAACCAACCGACTGCCACGACGAGCAATCCCAAAAGT 180
Db 121 TTGCTTGCAGGGCTGAACCAACCGACTGCCACGAGCAATCCCAAAAGT 180
QY 181 GGGCATCCCTGTTTGTACCGAGTACCACCGGGGCTGAACACTCCCTGGCAGCGGGCG 240
Db 181 GGGCATCCCTGTTTGTACCGAGTACCACCGGGGCTGAACACTCCCTGGCAGCGGGCG 240
QY 241 AAGCGTGCACACACTGCAATTTTAAGACACAAATTGAAGTGGCACAGTATGGCACAC 300
Db 241 AAGCGTGCACACACTGCAATTTTAAGACACAAATTGAAGTGGCACAGTATGGCACAC 300
QY 301 AATAGCCATTAACGTTGAGAGGTTGAGATGGCACACAGCTAGCGAACAATTAATGACA 360
Db 301 AATAGCCATTAACGTTGAGAGGTTGAGATGGCACACAGCTAGCGAACAATTAATGACA 360
QY 361 CTTTGGAGCTCAAGGTTGAAGCGAATTTATGTTGTGGGTGACAGCTTAATCCGA 420
Db 361 CTTTGGAGCTCAAGGTTGAAGCGAATTTATGTTGTGGGTGACAGCTTAATCCGA 420
QY 421 TCGTGATGCTGTCCGCCAATCAGATATTGATGGGTGACAGTTCGAATAGGAAAGCG 480
Db 421 TCGTGATGCTGTCCGCCAATCAGATATTGATGGGTGACAGTTCGAATAGGAAAGCG 480
QY 481 CGGCGTTTGCAGCCCGTCCGGAATCGTATCTACTGCGAGCTGGCAGTATGCTGCTT 540
Db 481 CGGCGTTTGCAGCCCGTCCGGAATCGTATCTACTGCGAGCTGGCAGTATGCTGCTT 540
QY 541 CTTTGGTCTGAGAACACACACCGATTCAGGGCTTATGATTCGATCGAATAGGTTG 600
Db 541 CTTTGGTCTGAGAACACACACCGATTCAGGGCTTATGATTCGATCGAATAGGTTG 600
QY 601 CGAAGCTGTGGCCATCCCTAGCCATATTCGAGTGCCAGATTGGTTGAGCTTCTCC 660
Db 601 CGAAGCTGTGGCCATCCCTAGCCATATTCGAGTGCCAGATTGGTTGAGCTTCTCC 660
QY 661 AGGAAGCGATCCCGAGATTTGTTTAAGGAATGCTGCTGATCTGCGAAGTGGTATG 720
Db 661 AGGAAGCGATCCCGAGATTTGTTTAAGGAATGCTGCTGATCTGCGAAGTGGTATG 720
QY 721 GTGCTGACAGGCTGAACGATTTTGCATCCAGCATTCAGTCCAGTGGCGGTAAAG 780
Db 721 GTGCTGACAGGCTGAACGATTTTGCATCCAGCATTCAGTCCAGTGGCGGTAAAG 780
QY 781 GTGCTGACAGGCTGAACGATTTTGCATCCAGCATTCAGTCCAGTGGCGGTAAAG 780
Db 781 GTGCTGACAGGCTGAACGATTTTGCATCCAGCATTCAGTCCAGTGGCGGTAAAG 780
QY 841 ATTCCATTCACATTTCTTCTGACACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Db 841 ATTCCATTCACATTTCTTCTGACACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
QY 901 CAGCGCTGTGGAGGCGATTAAACAGCTAGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
Db 901 CAGCGCTGTGGAGGCGATTAAACAGCTAGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
QY 961 TGAAGAATGCTGCGCGAGGCTGTTGAGGTTGGGGAAGAATTAATCACCGATCGGCG 1020
Db 961 TGAAGAATGCTGCGCGAGGCTGTTGAGGTTGGGGAAGAATTAATCACCGATCGGCG 1020
QY 1021 ATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
Db 1021 ATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
QY 1081 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
Db 1081 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
QY 1141 TGGTACGATTTCTCTATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1200
Db 1141 TGGTACGATTTCTCTATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1200

Db	1141	1GGGTACGGATTTCCCTATTCTGATTTCTCTCTTAAGAACAAGTTGCCAGTGGATA	1200
QY	1201	TCAACGCTGGCACATTGGTCTGCAGCTAACACGGTGAAGTATCCGGTGCACGGTGAATTTG	1260
Db	1201	TCAACGGTGGCACATTGGTGCAGCTAACACGGTGAAGTATCCGGTGCACGGTGAATTTG	1260
QY	1261	CTCAGCAAAATCGAAAATATTTTGCTATGTGAAAGGAAAAACAGATCGTTCTCTCTTG	1320
Db	1261	CTGCACAAATCGAAAATATTTTTCCTCATGTGAAAGGAAAAACAGATCGTTCTCTCTTG	1320
QY	1321	ATCGATGCTCAAAGGCACACGACGTAACTTGAGCTCGGTGTAGAGACGTACACACATA	1380
Db	1321	ATCGATGCTCAAAGGCACACGACGTAACTTGAGCTCGGTGTAGAGACGTACACACATA	1380
QY	1381	ACGTCGAGAGCAATGTGTCCTATTCACCCCTGAATAAGTGTGCTCATTTTGAACAGCTGG	1440
Db	1381	ACGTCGAGAGCAATGTGTCCTATTCACCCCTGAATAAGTGTGCTCATTTTGAACAGCTGG	1440
QY	1441	CGGATAAGATGGCGGTGTTTACTGTGATACCGGCATGTGCATGTGTGTCATGCGAGT	1500
Db	1441	CGGATAAGATGGCGGTGTTTACTGTGATACCGGCATGTGCATGTGTGTCATGCGAGT	1500
QY	1501	ACATCGAGATCCGGAGGAGAACGGCAGCTTTGGGGTTCATTCGCCACAGCGACGATGG	1560
Db	1501	ACATCGAGATCCGGAGGAGAACGGCAGCTTTGGGGTTCATTCGCCACAGCGACGATGG	1560
QY	1561	CTAATGCGTTGCCCTCATGCGATTGTGTGCGCAAAAGTGTGATCGAAACCGCAGGTGATCG	1620
Db	1561	CTAATGCGTTGCCCTCATGCGATTGTGTGCGCAAAAGTGTGATCGAAACCGCAGGTGATCG	1620
QY	1621	CGATGTGTGGCGATGTGTGTGTTTGGGGCATGTGCTGCGGTGAGCTTGTCTAACCCTTAAGCTGC	1680
Db	1621	CGATGTGTGGCGATGTGTGTGTTTGGGGCATGTGCTGCGGTGAGCTTGTCTAACCCTTAAGCTGC	1680
QY	1681	ACCAACTTTCGCGTGAAGGCTGTGTGTGTTTAAACAACAGTTCTTTGGGCAATGGTCAAGTTGG	1740
Db	1681	ACCAACTTTCGCGTGAAGGCTGTGTGTGTTTAAACAACAGTTCTTTGGGCAATGGTCAAGTTGG	1740
QY	1741	AGATGCTCTGTGAGAGGACACGCCAATTTTGGTACTGACCATGAGAGAAGTGATTTCCGAG	1800
Db	1741	AGATGCTCTGTGAGAGGACACGCCAATTTTGGTACTGACCATGAGAGAAGTGATTTCCGAG	1800
QY	1801	AGATTGGGGGGCTGCGGGTATCAAAATCGGTACCGATCACCGATCCGAGAGAAATTTGGCG	1860
Db	1801	AGATTGGGGGGCTGCGGGTATCAAAATCGGTACCGATCACCGATCCGAGAGAAATTTGGCG	1860
QY	1861	AGCAGCTAGCTGAGAGCATTTGGCATATCTCTGACCTGTACATGTGATGATGTCACGGATC	1920
Db	1861	AGCAGCTAGCTGAGAGCATTTGGCATATCTCTGACCTGTACATGTGATGATGTCACGGATC	1920
QY	1921	CTAATGCGCTGTGCATCCCAACAACATCAAGTGTGGAACAGGTATGAGATTCAGCAAGG	1980
Db	1921	CTAATGCGCTGTGCATCCCAACAACATCAAGTGTGGAACAGGTATGAGATTCAGCAAGG	1980
QY	1981	CGGCGACCCGACCGCTCTTTGTGTGAGSAGTAGAGAGGATGATGATCTGGCCGTTGCA	2040
Db	1981	CGGCGACCCGACCGCTCTTTGTGTGAGSAGTAGAGAGGATGATGATCTGGCCGTTGCA	2040
QY	2041	ACATAAGAAATATCTACTCATGATGATGTGATACACGTGCTTCTTCATTTGACCGGGA	2100
Db	2041	ACATAAGAAATATCTACTCATGATGATGTGATACACGTGCTTCTTCATTTGACCGGGA	2100
QY	2101	GGCGTTAATCTGCCAACAATTTTCAGAGATGGCAGCTCACGCCGTGCCATGAGATGGCCT	2160
Db	2101	GGCGTTAATCTGCCAACAATTTTCAGAGATGGCAGCTCACGCCGTGCCATGAGATGGCCT	2160

RESULT 5
ABL58754
ID ABL58754 standard; DNA; 2160 BP.

AC ABL58754;
XX

DT	05-JUL-2002 (first entry)	
XX	Corynebacterium poxB encoding polynucleotide SEQ ID NO 1.	
DE		
XX	Corynebacterium; poxB; pyruvate oxidase; enzyme; fermentative production;	
KW	D-pantothenic acid; vitamin; medicine; pharmaceutical; food industry;	
KW	animal nutrition; gene; ds.	
XX		
OS	Corynebacterium glutamicum.	
XX		
XX	Key	Location/Qualifiers
FT	-35_signal	227..232
FT		/*tag= a
FT	-10_signal	256..261
FT		/*tag= b
FT	CDS	327..2066
FT		/*tag= c
FT		/product= "poxB"
FT		/EC_number= "1.2.2.2"
XX		
EN	DE10117085-A1.	
XX		
PD	11-APR-2002.	
XX		
XX	06-APR-2001; 2001DE-1017085.	
PF		
XX	30-SEP-2000; 2000DE-1048604.	
PR		
XX	(DEGS) DEGUSA AG.	
PA		
XX	Dusch N, Herrmann T, Thierbach G;	
PI		
XX	WPI: 2002-363950/40.	
DR	P-PSDB; ABB79447.	
DR		
XX		
XX	Fermentative production of D-pantothenic acid (I), useful e.g. in	
PT	animal nutrition, from coryneform bacteria with reduced activity of the	
PT	pyruvate oxidase gene -	
XX		
PS	Claim 13; Page 11-14; 28pp; German.	
XX		
CC	The invention relates to the fermentative production of D-pantothenic	
CC	acid (I) by growing a (I)-producing coryneform bacterium in which the	
CC	activity of at least the sequence poxB (AB158754, AB158756) encoding	
CC	pyruvate oxidase (AB58755, EC 1.2.2.2) has been weakened, especially	
CC	switched off. (I) is then recovered from medium or cells. (I) is a	
CC	vitamin useful in human medicine, the pharmaceutical and food industries	
CC	and particularly in animal nutrition. Reducing the activity of poxB	
CC	improves fermentative production of (I).	
XX		
SO	Sequence 2160 BP; 491 A; 486 C; 647 G; 536 T; 0 other;	
	Query Match	100.0%; Score 2160; DB 24; Length 2160;
	Best Local Similarity	100.0%; Pred. No. 0;
	Matches 2160; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1 TTAGAGCGGATTTCTGTGAGTCACTTTTGTGGGGTGGGGCTTAAATTGGCCAGTTT	60
DB	1 TTAGAGCGGATTTCTGTGAGTCACTTTTGTGGGGTGGGGCTTAAATTGGCCAGTTT	60
QY	CGAGGCGGACGACAGAGGGGTGCCACGATGTTTAAATGGGATCGGGGCGATCTGTGT	120
DB	61 CGAGGCGGACGACAGAGGGGTGCCACGATGTTTAAATGGGATCGGGGCGATCTGTGT	120
QY	121 TTGGTTTGCAGGGGCTGAAACCAACGACGACTGCGCCACGACGAGGAAATCCCAAAAGT	180
DB	121 TTGGTTTGCAGGGGCTGAAACCAACGACGACTGCGCCACGACGAGGAAATCCCAAAAGT	180
QY	181 GGGGATCCCTTTTGTGTACCGAGTACCCACCGGGGCTGAAATCTCCCTGGAGGGGGGCG	240
DB	181 GGGGATCCCTTTTGTGTACCGAGTACCCACCGGGGCTGAAATCTCCCTGGAGGGGGGCG	240
QY	241 AAGCGTGCAACACTGGAATTTAAGACACATTTGAAGTGGACCAAGTTAGGCAACAC	300

Db 241 AAGGTGGCAACACTGGATTTAAGGCAATGTGAAGTCGACCCAGTATGGCAACAC 300
QY 301 AATAGCCATACGTTGAGAGGTTGAGATGGCACACAGCTACGAGAACTTAATGACA 360
Db 301 AATAGCCATACGTTGAGAGGTTGAGATGGCACACAGCTACGAGAACTTAATGACA 360
QY 361 CTTTGAAGCTCAAGGTGTAAGCAATTTATGTTGGTGGGTGACAGCCTTAATCGA 420
Db 361 CTTTGAAGCTCAAGGTGTAAGCAATTTATGTTGGTGGGTGACAGCCTTAATCGA 420
QY 421 TCGTGATGCTGTCCGCCAATCAGATATTGATGGGTGACGTTCCGAATGAGAAAGCG 480
Db 421 TCGTGATGCTGTCCGCCAATCAGATATTGATGGGTGACGTTCCGAATGAGAAAGCG 480
QY 481 CGGCGTTTGACAGCGGTGCGGAATCCTGATCAGTGGGAGCTGGCAGTATGTCTTC 540
Db 481 CGGCGTTTGACAGCGGTGCGGAATCCTGATCAGTGGGAGCTGGCAGTATGTCTTC 540
QY 541 CTTGTGCTGTGAAACACACACACCTGATTCAGGCTTTATGATTCGCATCGAAATGCTG 600
Db 541 CTTGTGCTGTGAAACACACACACCTGATTCAGGCTTTATGATTCGCATCGAAATGCTG 600
QY 601 CGAAGGTGTTGGCCATCGCTAGCCATATCCAGATGCCAGATTGGTTCAGCTTCTCC 660
Db 601 CGAAGGTGTTGGCCATCGCTAGCCATATCCAGATGCCAGATTGGTTCAGCTTCTCC 660
QY 661 AGGAACGATCGGAGATTTGTTTAAAGAAATGCTCTGTTACTCGAGATGTTAATG 720
Db 661 AGGAACGATCGGAGATTTGTTTAAAGAAATGCTCTGTTACTCGAGATGTTAATG 720
QY 721 GTGTGAGCAGGAGTGAACGATTTTGATCAGCGCGATGATGATCAGATGGGCGGTAAG 780
Db 721 GTGTGAGCAGGAGTGAACGATTTTGATCAGCGCGATGATGATCAGATGGGCGGTAAG 780
QY 781 GTGTGCGGTGATGATTCCTGATGATGCTTAAGGAAGCAGAGTGAAGTACTT 840
Db 781 GTGTGCGGTGATGATTCCTGATGATGCTTAAGGAAGCAGAGTGAAGTACTT 840
QY 841 ATTTCAATTCACACTATTTCTGTGACCTCTGTGTCTCCGAGTCTTACTGAGCGTG 900
Db 841 ATTTCAATTCACACTATTTCTGTGACCTCTGTGTCTCCGAGTCTTACTGAGCGTG 900
QY 901 CAGCGGTGAGAGCGATTAAACAACGCTAGTCTGTCTTGTCTCGGTCGCGGCG 960
Db 901 CAGCGGTGAGAGCGATTAAACAACGCTAGTCTGTCTTGTCTCGGTCGCGGCG 960
QY 961 TGAAGAATGCTCGCGCGAGGTGTTGAGATGGCGAGAAATTAATCACCAGATCGGCG 1020
Db 961 TGAAGAATGCTCGCGCGAGGTGTTGAGATGGCGAGAAATTAATCACCAGATCGGCG 1020
QY 1021 ATGCCCTGGGTGATGAGCAGTACATCCAGCATGAGATCCGTTTGAAGGTGAGATGCTG 1080
Db 1021 ATGCCCTGGGTGATGAGCAGTACATCCAGCATGAGATCCGTTTGAAGGTGAGATGCTG 1080
QY 1081 GCCTCTGTTGATGAGCGGCTGCTGATGCTCCCAATGAGCGGATCTGATTTCTAT 1140
Db 1081 GCCTCTGTTGATGAGCGGCTGCTGATGCTCCCAATGAGCGGATCTGATTTCTAT 1140
QY 1141 TGGGTAGGATTTCCCTATCTGATTTCTTCTTAAAGACACAGTTCGCCAGGTGATA 1200
Db 1141 TGGGTAGGATTTCCCTATCTGATTTCTTCTTAAAGACACAGTTCGCCAGGTGATA 1200
QY 1201 TCAAGGTGCGCACATTTGTCGACGTACACAGTAAATCCGTTGAGCGGTCGATGTTG 1260
Db 1201 TCAAGGTGCGCACATTTGTCGACGTACACAGTAAATCCGTTGAGCGGTCGATGTTG 1260
QY 1261 CTGCAACATCGAAATATTTTCTCATGTGAAGGAAAAACAGATGTTCTCTCTTG 1320
Db 1261 CTGCAACATCGAAATATTTTCTCATGTGAAGGAAAAACAGATGTTCTCTCTTG 1320
QY 1321 ATCGATGCTCAAGGACAGAGGTAGTGTGCTGCTGATGACGATACACATA 1380
Db 1321 ATCGATGCTCAAGGACAGAGGTAGTGTGCTGCTGATGACGATACACATA 1380

Db 1321 ATCGATGCTCAAGGACAGAGGTAGTGTGCTGCTGATGACGATACACATA 1380
QY 1381 ACGTCGAGAGCATGTGCTATTACCCCTGATACGTTGGCTCTATTGTAACAGCTGG 1440
Db 1381 ACGTCGAGAGCATGTGCTATTACCCCTGATACGTTGGCTCTATTGTAACAGCTGG 1440
QY 1441 CGGATTAAGGATGCGGTTTACTGTGATACCGCATGTGCAATGTGTGCGATCGAGT 1500
Db 1441 CGGATTAAGGATGCGGTTTACTGTGATACCGCATGTGCAATGTGTGCGATCGAGT 1500
QY 1501 ACATCGAGATTCGCGAGGGAACGCGCATTTGTGGGTTCAATCCGCCACGCAAGATG 1560
Db 1501 ACATCGAGATTCGCGAGGGAACGCGCATTTGTGGGTTCAATCCGCCACGCAAGATG 1560
QY 1561 CTATGCGTGGCCATGAGCATTTGTCGGAAGATGTCGAATCCGAACCCGAGTATG 1620
Db 1561 CTATGCGTGGCCATGAGCATTTGTCGGAAGATGTCGAATCCGAACCCGAGTATG 1620
QY 1621 CGATGTGTGCGATGATGTTTGGGATGCTGCTGGGTGAGCTTCTGACCTTAAAGCTGC 1680
Db 1621 CGATGTGTGCGATGATGTTTGGGATGCTGCTGGGTGAGCTTCTGACCTTAAAGCTGC 1680
QY 1681 ACCAATTCGCGTGAAGGCTGTGTTTAAACAAGTCTTTGGGATGAGTAAATTCG 1740
Db 1681 ACCAATTCGCGTGAAGGCTGTGTTTAAACAAGTCTTTGGGATGAGTAAATTCG 1740
QY 1741 AGATGCTGCTGAGGAGACACAGAAATTTGTAAGTACATGAGAGAGTAAATTCG 1800
Db 1741 AGATGCTGCTGAGGAGACACAGAAATTTGTAAGTACATGAGAGAGTAAATTCG 1800
QY 1801 AGATGCTGCTGAGGAGTATCAATGCTGATGATGATGATGATGATGATGATGATG 1860
Db 1801 AGATGCTGCTGAGGAGTATCAATGCTGATGATGATGATGATGATGATGATGATG 1860
QY 1861 AGCAGTATGCTGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 1920
Db 1861 AGCAGTATGCTGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 1920
QY 1921 CTATGCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1980
Db 1921 CTATGCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1980
QY 1981 CGGCGACCCGGAACCGCTTTTGTGAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 2040
Db 1981 CGGCGACCCGGAACCGCTTTTGTGAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 2040
QY 2041 ACATAGGATATTTCTTACCTCATGATGATGATGATGATGATGATGATGATGATG 2100
Db 2041 ACATAGGATATTTCTTACTCATGATGATGATGATGATGATGATGATGATGATG 2100
QY 2101 GCGCTTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2160
Db 2101 GCGCTTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2160

RESULT 6
ABL58756
ID ABL58756 standard; DNA; 3248 bp.
XX ABL58756;
AC XX
XX XX
DT 05-JUL-2002 (first entry)
XX
DE Corynebacterium poxb encoding polynucleotide seq id NO 4.
XX
XX Corynebacterium: poxb: pyruvate oxidase; enzyme: fermentative production;
KW D-pantothenic acid; vitamin; medicine; pharmaceutical; food industry;
KW animal nutrition; gene; ds.
XX
XX
OS Corynebacterium glutamicum.
XX
XX
FH Key
CDS Location/Qualifiers
802..2541

```

FT      /*tag= c
FT      /product= "poxb"
FT      /EC_number= "1.2.2.2"
XX
XX
XX      DE10117085-A1.
XX
XX      11-APR-2002.
XX
XX      06-APR-2001; 2001DE-1017085.
XX
XX      30-SEP-2000; 2000DE-1048604.
XX
XX      (DEGS ) DEGUSSA AG.
XX
XX      Dusch N, Herrmann T, Thierbach G;
XX
XX      WPI: 2002-363950/40.
XX      P-PSDB: ABB79447.
XX
XX      Fermentative production of D-pantothenic acid (I), useful e.g. in
XX      animal nutrition, from coryneform bacteria with reduced activity of the
XX      pyruvate oxidase gene -
XX
XX      Example 4; Page 16-20; 28pp; German.
XX
XX      The invention relates to the fermentative production of D-pantothenic
XX      acid (I) by growing a (I)-producing coryneform bacterium in which the
XX      activity of at least the sequence poxb (AB158754, AB158756) encoding
XX      pyruvate oxidase (AB158755, EC 1.2.2.2) has been weakened, especially
XX      switched off. (I) is then recovered from medium or cells. (I) is a
XX      vitamin useful in human medicine, the pharmaceutical and food industries
XX      and particularly in animal nutrition. Reducing the activity of poxb
XX      improves fermentative production of (I).
XX
XX      Sequence 3248 BP; 744 A; 743 C; 985 G; 776 T; 0 other;
XX
XX      Query Match      100.0%; Score 2160; DB 24; Length 3248;
XX      Best Local Similarity 100.0%; Pred. No. 0;
XX      Matches 2160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      QY      1 TTAAGGCGATTCTGTGTAGGTCACATTTTGTGGGGTGGGGTCTAAATTTGGCCAGTTT 60
XX      DB      476 TTAAGGCGATTCTGTGTAGGTCACATTTTGTGGGGTGGGGTCTAAATTTGGCCAGTTT 535
XX
XX      QY      61 CGAGGCGACGACAGGCGTGCCCGCATGTTAAATAGGCGATCGGGCATCTGTGT 120
XX      DB      536 CGAGGCGACGACAGGCGTGCCCGCATGTTAAATAGGCGATCGGGCATCTGTGT 595
XX
XX      QY      121 TTGGTTTCGAGCGGGCTGAACCAACAGAGACTGCCAGCAAGCAAGCAATCCCAAAAGT 180
XX      DB      596 TTGGTTTCGAGCGGGCTGAACCAACAGAGACTGCCAGCAAGCAAGCAATCCCAAAAGT 655
XX
XX      QY      181 GGGCATCCCTGTGTGTACGAGTACCCACCCGGGCTGAACCTCCCTGGCAGGCGGGCG 240
XX      DB      656 GGGCATCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 715
XX
XX      QY      241 AAGGTGGCAACAACACTGGAATTTAGAGCAATTTAGTGCGCAAGTAAAGTAAAGCAAC 300
XX      DB      716 AAGGTGGCAACAACACTGGAATTTAGAGCAATTTAGTGCGCAAGTAAAGTAAAGCAAC 775
XX
XX      QY      301 AATAGCATATAGCTTGAGAGGTTGAGTGCACACAGCTACGCGAAGCAATTAATTGACA 360
XX      DB      776 AATAGCATATAGCTTGAGAGGTTGAGTGCACACAGCTACGCGAAGCAATTAATTGACA 835
XX
XX      QY      361 CTTTGAAGGTCAAGGTGTAAGCGAATTTATGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
XX      DB      836 CTTTGAAGGTCAAGGTGTAAGCGAATTTATGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 895
XX
XX      QY      421 TCGTGATGCTGTCCCGCAATCAGATATTAGTGGGTGCAGTTTCGAATGAGAGAGCGG 480
XX      DB      896 TCGTGATGCTGTCCCGCAATCAGATATTAGTGGGTGCAGTTTCGAATGAGAGAGCGG 955
XX
XX      QY      481 CGGCGTTTGACGCGGTGCGGAATCGTTGATCACTGGGAGCTGGCAGTATGTCTGCTT 540

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DB      956 CGGCGTTTGACGCGGTGCGGAATCGTTGTACTGTGGGAGTGGCAGTATGTCTGCTT 1015
XX
XX      QY      541 CTTGTGCTCTGGAACACACACACTGATTCAGGCTCTTTATGTTGCGATCGAAATGCTG 600
XX      DB      1016 CTTGTGCTCTGGAACACACACACTGATTCAGGCTCTTTATGATTCGATCGAAATGCTG 1075
XX
XX      QY      601 CGAAGGTGTGGCATCGTAGCATATTCGAGTCCGACGATTTGGTTCACGTTCTTC 660
XX      DB      1076 CGAAGGTGTGGCATCGTAGCATATTCGAGTCCGACGATTTGGTTCACGTTCTTC 1135
XX
XX      QY      661 AGGAAAGCATCCCGGAGATTTTGTTAAGGAATCTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
XX      DB      1136 AGGAAAGCATCCCGGAGATTTTGTTAAGGAATCTGTGTGTGTGTGTGTGTGTGTGTGTGT 1195
XX
XX      QY      721 GTGGTAGAGGAGGTGTAACCATTTTTCATTCACCGGATTAAGTCCACCATGGCGGTAAAG 780
XX      DB      1196 GTGGTAGAGGAGGTGTAACCATTTTTCATTCACCGGATTAAGTCCACCATGGCGGTAAAG 1255
XX
XX      QY      781 GTGTGTGCTGTAGTATTCCTGCTGATATCGCTAAGGAAAGACGAGGTGAGCTACTT 840
XX      DB      1256 GTGTGTGCTGTAGTATTCCTGCTGATATCGCTAAGGAAAGACGAGGTGAGCTACTT 1315
XX
XX      QY      841 ATTCGAATTCACATATTCTCTGTGACACTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
XX      DB      1316 ATTCGAATTCACATATTCTCTGTGACACTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1375
XX
XX      QY      901 CAGCGCTGTGAGGCGATTAACAAGCGTAATCTGTACTTTGTCTGTGTGTGTGTGTGTGTGTGT 960
XX      DB      1376 CAGCGCTGTGAGGCGATTAACAAGCGTAATCTGTACTTTGTCTGTGTGTGTGTGTGTGTGTGT 1435
XX
XX      QY      961 TGAAGAAATCTGCGCGCGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1020
XX      DB      1436 TGAAGAAATCTGCGCGCGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1495
XX
XX      QY      1021 ATGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1080
XX      DB      1496 ATGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1555
XX
XX      QY      1081 GCGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1140
XX      DB      1556 GCGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1615
XX
XX      QY      1141 TTGGTAGGATTTCCCTTATTCGTATTTCTTCTTAAGACAACTGGCCAGTGTGATA 1200
XX      DB      1616 TTGGTAGGATTTCCCTTATTCGTATTTCTTCTTAAGACAACTGGCCAGTGTGATA 1675
XX
XX      QY      1201 TCAAGGTGCGCACATTTGTGAGCTACCAAGGTGAAGTATCCGGTGAACGGTGTATGTTG 1260
XX      DB      1676 TCAAGGTGCGCACATTTGTGAGCTACCAAGGTGAAGTATCCGGTGAACGGTGTATGTTG 1735
XX
XX      QY      1261 CTGCAACATCGAAATATTTTGTGCTCATGTGTGAAGGAAACACATGTTCTTCTCTTG 1320
XX      DB      1736 CTGCAACATCGAAATATTTTGTGCTCATGTGTGAAGGAAACACATGTTCTTCTCTTG 1795
XX
XX      QY      1321 ATCGGATGCTGAAGGACACGAGCGTAAGTTGAGCTCGGTGTAGAGAGCTACACACATA 1380
XX      DB      1796 ATCGGATGCTGAAGGACACGAGCGTAAGTTGAGCTCGGTGTAGAGAGCTACACACATA 1855
XX
XX      QY      1381 ACGTGAAGCAATGTGCTATTTCACCTGTAATACGTTGCTCTTATTTTGAACGAGCTGG 1440
XX      DB      1856 ACGTGAAGCAATGTGCTATTTCACCTGTAATACGTTGCTCTTATTTTGAACGAGCTGG 1915
XX
XX      QY      1441 CGGATTAAGGATGCGGTGTCTCTGTGTATCCGAGATGTGAATGTGGGATGGGAGGT 1500
XX      DB      1916 CGGATTAAGGATGCGGTGTCTCTGTGTATCCGAGATGTGAATGTGGGATGGGAGGT 1975
XX
XX      QY      1501 ACATCGAATCGGAGGAAAGCGCGCATTTTGTGGTTCAATTCGCGACGCGACGATG 1560
XX      DB      1976 ACATCGAATCGGAGGAAAGCGCGCATTTTGTGGTTCAATTCGCGACGCGACGATG 2035
XX
XX      QY      1561 CTATATGCTGCTCAATGCGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1620

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Db 2036 CTAATGGCTTCCCTCATGCGATTGTGCGCAAGTGTGTGATCGAAGCCGCCAGGTGATCG 2095
QY 1621 CGATGTGTGGCGATGGTGGTGGGATGCTGCTGGGTGAGCTTCTGACCGTTAAAGCTGC 1680
Db 2096 CGATGTGTGGCGATGGTGGTGGGATGCTGCTGGGTGAGCTTCTGACCGTTAAAGCTGC 2155
QY 1681 ACCAATCTCCGCTGAACCGCTGTGTGTAAACAAGTCTTGTGGCATGTGTGAAGTTGG 1740
Db 2156 ACCAATCTCCGCTGAACCGCTGTGTGTAAACAAGTCTTGTGGCATGTGTGAAGTTGG 2215
QY 1741 AGATGCTCTGTGGAGGAGACCGCAAGATTGTGTCTGACATGAGGAAGTGAATTTGGCAG 1800
Db 2216 AGATGCTCTGTGGAGGAGACCGCAAGATTGTGTCTGACATGAGGAAGTGAATTTGGCAG 2275
QY 1801 AGATGCTCTGTGGAGGAGACCGCAAGATTGTGTCTGACATGAGGAAGTGAATTTGGCAG 1860
Db 2276 AGATGCTCTGTGGAGGAGACCGCAAGATTGTGTCTGACATGAGGAAGTGAATTTGGCAG 2335
QY 1861 AGCAGCTAGCTGAGGCAATTTGGCATATCTCTGACCTGACTGATGATGATGTCAGGATC 1920
Db 2336 AGCAGCTAGCTGAGGCAATTTGGCATATCTCTGACCTGACTGATGATGATGTCAGGATC 2395
QY 1921 CTAATGGCTTCCCTCATGCGATTGTGCGCAAGTGTGTGATCGAAGCCGCCAGGTGATCG 1980
Db 2396 CTAATGGCTTCCCTCATGCGATTGTGCGCAAGTGTGTGATCGAAGCCGCCAGGTGATCG 2455
QY 1981 CGGCGACCCGACCGCTTTTGTGTGGAGAGTAGAGAGCGATGATGATCTGGCCGTTTGA 2040
Db 2456 CGGCGACCCGACCGCTTTTGTGTGGAGAGTAGAGAGCGATGATGATCTGGCCGTTTGA 2515
QY 2041 ACATAGAGAAATATCTCTACTCTCATGATGATGATGATGATGATGATGATGATGATG 2100
Db 2516 ACATAGAGAAATATCTCTACTCTCATGATGATGATGATGATGATGATGATGATGATG 2575
QY 2101 GCGCTTAATCTGCAACATCTTCCAGAGATGCGAGCTCAGCGCGGTGCCATGAGTGGCCT 2160
Db 2576 GCGCTTAATCTGCAACATCTTCCAGAGATGCGAGCTCAGCGCGGTGCCATGAGTGGCCT 2635

RESULT 7

AAH68533/c
ID AAH68533 standard; DNA; 349980 BP.

AAH68533;

26-SEP-2001 (first entry)

C glutamicum coding sequence fragment SEQ ID NO: 7068.

Coriiform bacterium; amino acid synthesis; vitamin; saccharide;

organic acid synthesis; ds.

Coriiform bacterium glutamicum.

EP1108790-A2.

20-JUN-2001.

18-DEC-2000; 2000EP-0127688.

16-DEC-1999; 99JP-0377484.

07-APR-2000; 2000JP-0159152.

03-AUG-2000; 2000JP-0280988.

(KYOWA) KYOWA HAKKO KOGYO KK.

Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;

Tateishi N, Senoh A, Ikeda M, Ozaki A;

WPI; 2001-376931/40.

Novel polynucleotides derived from Coriiform bacteria, for identifying

mutation point of a gene, measuring expression of a gene, analysing

PT expression profile or pattern of a gene and identifying homologous gene
PT
XX
PS Disclosure: SEQ ID NO: 7068; 246pp + Sequence Listing; English.
CC The present invention provides a number of nucleotide and protein
CC sequences from the Coriiform bacterium Coriiform bacterium glutamicum. These
CC are useful for identifying the mutation point of a gene derived from a
CC mutant of coriiform bacterium, measuring expression amount and
CC analysing the expression profile or expression pattern of a gene derived
CC from Coriiform bacterium, and identifying a homologue of a gene derived
CC from Coriiform bacterium. Coriiform bacteria are useful for producing
CC amino acids, nucleic acids, vitamins, saccharides and organic acids,
CC particularly L-lysine. The present sequence is a nucleic acid described
CC in the exemplification of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from the
CC European Patent Office.
XX
XX

Sequence 349980 BP; 81250 A; 97718 C; 90621 G; 80391 T; 0 other;

Query Match 100.0%; Score 2160; DB 22; Length 349980;

Best local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 2160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGAGCGCATCTCTGTGAGTCACTTTTGTGGGTGCGGGCTTAATTTGGCCAGTTT 60
Db 78830 TTAGAGCGCATCTCTGTGAGTCACTTTTGTGGGTGCGGGCTTAATTTGGCCAGTTT 78771
QY 61 CGAGGCGACACAGACGCGTGCACGATGTTTAATAGCGCATGGTGGGATCTGTGT 120
Db 78770 CGAGGCGACACAGACGCGTGCACGATGTTTAATAGCGCATGGTGGGATCTGTGT 78711
QY 121 TTGGTTTGACGCGCTGAACCAACCAACAGACTGCCAGACAGACGAGGAATCCAAAGT 180
Db 78710 TTGGTTTGACGCGCTGAACCAACCAACAGACTGCCAGACAGACGAGGAATCCAAAGT 78651
QY 181 GGGCATCCCTGTTTGTGACGATCCACCGCGGCGCTGAAGTCCCTGGCGAGGCGCG 240
Db 78650 GGGCATCCCTGTTTGTGACGATCCACCGCGGCGCTGAAGTCCCTGGCGAGGCGCG 78591
QY 241 AAGCGTGGCAACACTGGAATTTAAGAGCACAATTTGAAGTGCACCAAGTTAAGCAAC 300
Db 78590 AAGCGTGGCAACACTGGAATTTAAGAGCACAATTTGAAGTGCACCAAGTTAAGCAAC 78531
QY 301 AATAGCCATTAACCTTGAAGAGTTCAGATGGCACAACGCTACCCAGCAATTAATTGACA 360
Db 78530 AATAGCCATTAACCTTGAAGAGTTCAGATGGCACAACGCTACCCAGCAATTAATTGACA 78471
QY 361 CTTTGAACCTCAAGGTGTGAAGCAATTTATGTTGTGGGTGACACACCTTAATCCGA 420
Db 78470 CTTTGAACCTCAAGGTGTGAAGCAATTTATGTTGTGGGTGACACACCTTAATCCGA 78411
QY 421 TCGTGATCCTGTCCGCCAATCAGATATTGAGTGGGTGACAGCTTGAATGAGAAGCGG 480
Db 78410 TCGTGATCCTGTCCGCCAATCAGATATTGAGTGGGTGACAGCTTGAATGAGAAGCGG 78351
QY 481 CGGCGTTTGCAGCGGTGCGGAATCGTTATGATCTAGTGGGAGTGGCAGATGTGCTGT 540
Db 78350 CGGCGTTTGCAGCGGTGCGGAATCGTTATGATCTAGTGGGAGTGGCAGATGTGCTGT 78291
QY 541 CTTGTGTCCTGGAACACACACACTGATTCAGGGTCTTTATGATTCGATCGAATGCTG 600
Db 78290 CTTGTGTCCTGGAACACACACACTGATTCAGGGTCTTTATGATTCGATCGAATGCTG 78231
QY 601 CGAAGGTGTGGCATCTGCTACGCAATTCGAGAGTGGCCAGATGGTTCGAGCTCTCC 660
Db 78230 CGAAGGTGTGGCATCTGCTACGCAATTCGAGAGTGGCCAGATGGTTCGAGCTCTCC 78171
QY 661 AGGAAAGCATCCGAGATTTTGTAAAGATGCTGTGTTACTGCGAGATGTAATG 720
Db 78170 AGGAAAGCATCCGAGATTTTGTAAAGATGCTGTGTTACTGCGAGATGTAATG 78111

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OY 721 GTGGTGGAGGAGTGAAGCATTGTCATCAGCGGATTCACCATGCGGGTAAAG 780
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DB 78110 GTGGTGGAGGAGTGAAGCATTGTCATCAGCGGATTCACCATGCGGGTAAAG 78051
OY 781 GTGTGTGGTGTAGTATGATTCCTGTGTATGCGTAAAGAGGAGGAGTACGCTACTT 840
    |||||||
DB 78050 GTGTGTGGTGTAGTATGATTCCTGTGTATGCGTAAAGAGGAGGAGTACGCTACTT 77991
OY 841 ATTCCAAATCCACATATTTCTTCTGCGACCTCTGTGGTGTGTCGGATCTTACTAGGCTG 900
    |||||||
DB 77990 ATTCCAAATCCACATATTTCTTCTGCGACCTCTGTGGTGTGTCGGATCTTACTAGGCTG 77931
OY 901 CAGCGCTGTGTGGAGGCGCATTAACACCGTAAAGTGTGCTGCTACTTGTGTCGGGTCGGGCG 960
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DB 77930 CAGCGCTGTGTGGAGGCGCATTAACACCGTAAAGTGTGCTGCTACTTGTGTCGGGTCGGGCG 77871
OY 961 TGAAGAAATGCTCGCGCGCGAGTGTGTGAGTGTGCGGAGAGATTAATACCGATCGGCGC 1020
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DB 77870 TGAAGAAATGCTCGCGCGCGAGTGTGTGAGTGTGCGGAGAGATTAATACCGATCGGCGC 77811
OY 1021 ATGCGCTGTGTGTAGAGAGTATCCAGATGAGAAATCCGTTGAGTGGGTCGATGCTGTG 1080
    |||||||
DB 77810 ATGCGCTGTGTGTAGAGAGTATCCAGATGAGAAATCCGTTGAGTGGGTCGATGCTGTG 77751
OY 1081 GCGTGTGTGTAGAGGCGCTGTGCGATGCTGCTCAATGAGGCGGATCTGCTGATCTAT 1140
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DB 77750 GCGTGTGTGTAGAGGCGCGCCGCGGTGATGCTGCTCAATGAGGCGGATCTGCTGATCTAT 77691
OY 1141 TGGGTAGCGATTTCCCTTATCTGATTTCCCTTAAAGACAGGTTGCCAGGTGATA 1200
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DB 77690 TGGGTAGCGATTTCCCTTATCTGATTTCCCTTAAAGACAGGTTGCCAGGTGATA 77631
OY 1201 TCACAGGTGCGCACATGTGTGCGACGTACCCAGGTGAAGTATCCGTTACCGGTTATGTTG 1260
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DB 77630 TCACAGGTGCGCACATGTGTGCGACGTACCCAGGTGAAGTATCCGTTACCGGTTATGTTG 77571
OY 1261 CTGCAACATGCAAAATATTTTGTGCTCATGTGAAGAAAAACAGATCGTTCCCTGCTTG 1320
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DB 77570 CTGCAACATGCAAAATATTTTGTGCTCATGTGAAGAAAAACAGATCGTTCCCTGCTTG 77511
OY 1321 ATCGGATGCTCAAGGCGACGACGAGGTGAAGTGTGAGCTCGGTGTGAGAGACGTACACATA 1380
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DB 77510 ATCGGATGCTCAAGGCGACGACGAGGTGAAGTGTGAGCTCGGTGTGAGAGACGTACACATA 77451
OY 1381 ACGTGGAGAACATGTGCTATTCATTCACCCCTGAATACGTTCCCTCTATTTGACAGAGCTGG 1440
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DB 77450 ACGTGGAGAACATGTGCTATTCATTCACCCCTGAATACGTTCCCTCTATTTGACAGAGCTGG 77391
OY 1441 CGGATTAAGCATGCGGTGTTTACTGTGTGATACCGGCAATGTGCAATGTGCGATCGAGGT 1500
    |||||||
DB 77390 CGGATTAAGCATGCGGTGTTTACTGTGTGATACCGGCAATGTGCAATGTGCGATCGAGGT 77331
OY 1501 ACATCGAATAATCCGAGGAGAACGCGGCACTTGTGGTTCATTTCCGCGACGCGCATGCG 1560
    |||||||
DB 77330 ACATCGAATAATCCGAGGAGAACGCGGCACTTGTGGTTCATTTCCGCGACGCGCATGCG 77271
OY 1561 CTAAATGCTGCTCATCATCATGATGTTGCGCAAAAGTGTGATGCAAAACGCGAGGTATGCG 1620
    |||||||
DB 77270 CTAAATGCTGCTCATCATCATGATGTTGCGCAAAAGTGTGATGCAAAACGCGAGGTATGCG 77211
OY 1621 CGATGTGTGCGGATGTGTGTTGGGCAATGCTGCTGGGTGAGCTTGTGACGTTAAAGCTGC 1680
    |||||||
DB 77210 CGATGTGTGCGGATGTGTGTTGGGCAATGCTGCTGGGTGAGCTTGTGACGTTAAAGCTGC 77151
OY 1681 ACCAACTTCCGCTTAAGGCTGTGTGTTTAAACACAGTCTTGTGGGATGTGTAAGTTGG 1740
    |||||||
DB 77150 ACCAACTTCCGCTTAAGGCTGTGTGTTTAAACACAGTCTTGTGGGATGTGTAAGTTGG 77091
OY 1741 AGATGCTGTGTGAGGAGACGCGCAATTTGGTACTGACCATGAGAGAAATGTAATTTCCAG 1800
    |||||||
DB 77090 AGATGCTGTGTGAGGAGACGCGCAATTTGGTACTGACCATGAGAGAAATGTAATTTCCAG 77031
OY 1801 AGATGCGGCGGTGCGGATATCAAAATCGGTACCATACCGCATCCGAAGAAATTTGCGG 1860

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DB 77030 AGATGCGGCGGTGCGGATATCAAAATCGGTACGATACCGGATCCGAAGAAATTCGCC 76971
OY 1861 AGCAGTACGCTGAGGAGCATTTGGCATATCTGAGACCTTACTGATGATGATTCGACGATC 1920
    |||||||
DB 76970 AGCAGTACGCTGAGGAGCATTTGGCATATCTGAGACCTTACTGATGATGATTCGACGATC 76911
OY 1921 CTAAATGCTGCTCATCATCATGATGTTGCGCAAAAGTGTGATGCAAAACGCGAGGTATGCG 1980
    |||||||
DB 76910 CTAAATGCTGCTCATCATCATGATGTTGCGCAAAAGTGTGATGCAAAACGCGAGGTATGCG 76851
OY 1981 CGGCGACCCGACACCGTCTTGTGTGAGAGATGAGAGATGATGATGATGATGATGATGATGATG 2040
    |||||||
DB 76850 CGGCGACCCGACACCGTCTTGTGTGAGAGATGAGAGATGATGATGATGATGATGATGATGATG 76791
OY 2041 ACATTAAGCAATATTTCTACTTCCATGATGATGATGATGATGATGATGATGATGATGATGATG 2100
    |||||||
DB 76790 ACATTAAGCAATATTTCTACTTCCATGATGATGATGATGATGATGATGATGATGATGATGATG 76731
OY 2101 GCGCTTACTGCGCACATTTCCAGATGAGGAGCTCAGCGCGGTGCCATGAGATGAGATGAGATG 2160
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DB 76730 GCGCTTACTGCGCACATTTCCAGATGAGGAGCTCAGCGCGGTGCCATGAGATGAGATGAGATG 76671

RESULT 8
AAF71402
ID AAF71402 standard; DNA; 1860 BP.
XX
AC AAF71402;
XX
DE 30-APR-2001 (first entry)
XX
DE Corynebacterium glutamicum SMP protein nucleotide sequence SEQ ID NO:85.
XX
KW Corynebacterium glutamicum; carbon metabolism and energy production;
KW SMP protein; sugar metabolism and oxidative phosphorylation protein;
KW fine chemical production; organic acid; proteinogenic amino acid;
KW nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside;
KW nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol;
KW carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme;
KW diagnosis; Corynebacterium diptheriae; evolutionary study; ds.
XX
OS Corynebacterium glutamicum.
XX
PN W0200100844-A2.
XX
PD 04-JAN-2001.
XX
PE 23-JUN-2000; 2000WC-IB00943.
XX
PR 25-JUN-1999; 99US-0141031.
PR 08-JUL-1999; 99DE-1031412.
PR 08-JUL-1999; 99DE-1031413.
PR 08-JUL-1999; 99DE-1031419.
PR 08-JUL-1999; 99DE-1031420.
PR 08-JUL-1999; 99DE-1031424.
PR 08-JUL-1999; 99DE-1031428.
PR 08-JUL-1999; 99DE-1031431.
PR 08-JUL-1999; 99DE-1031433.
PR 08-JUL-1999; 99DE-1031434.
PR 08-JUL-1999; 99DE-1031510.
PR 08-JUL-1999; 99DE-1031562.
PR 08-JUL-1999; 99DE-1031634.
PR 09-JUL-1999; 99DE-1032180.
PR 09-JUL-1999; 99DE-1032227.
PR 09-JUL-1999; 99DE-1032230.
PR 09-JUL-1999; 99US-0143208.
PR 14-JUL-1999; 99DE-1032924.
PR 14-JUL-1999; 99DE-1032973.
PR 14-JUL-1999; 99DE-1033005.
PR 27-AUG-1999; 99DE-1040765.
PR 31-AUG-1999; 99US-0151572.
PR 03-SEP-1999; 99DE-1042076.

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PR 03-SEP-1999; 99DE-1042079.
 PR 03-SEP-1999; 99DE-1042086.
 PR 03-SEP-1999; 99DE-1042087.
 PR 03-SEP-1999; 99DE-1042088.
 PR 03-SEP-1999; 99DE-1042095.
 PR 03-SEP-1999; 99DE-1042123.
 PR 03-SEP-1999; 99DE-1042125.
 XX
 PA (BADI) BASF AG.
 XX
 PI Pompeius M, Kroegeer B, Schroeder H, Zelder O, Haberhauer G;
 XX WFI; 2001-061975/07.
 DR P-PSDB; AAB79285.
 XX
 PT New isolated Corynebacterium glutamicum nucleic acid encoding a sugar
 PT metabolism and oxidative phosphorylation protein for production or
 PT modulation of production of fine chemicals e.g. amino acids,
 PT carbohydrates or enzymes -
 XX
 PS Claim 3; Page 268-270; 1246pp; English.
 XX
 CC AAF71360 to AAF71750 encode the Corynebacterium glutamicum sugar
 CC metabolism and oxidative phosphorylation (SMP) proteins given in
 CC AAB79243 to AAB 79633 which are involved in carbon metabolism and
 CC energy production. The C. glutamicum SMP gene can be used in vectors
 CC (II) for expression in host cells and production or modulation of
 CC production of fine chemicals, such as, an organic acid, a proteogenic
 CC or nonproteogenic amino acid (preferred), a purine or pyrimidine base,
 CC a nucleoside, a nucleotide, a lipid, a saturated or unsaturated fatty
 CC acid, a diol, a carbohydrate, an aromatic compound, a vitamin, a
 CC cofactor, a polyketide, or an enzyme. The presence of (I) or SMP proteins
 CC (III) encoded by them are used for diagnosing the presence or activity of
 CC Corynebacterium diptheriae in a subject. (I), (II), (III) or host cells
 CC containing them are used to map genomes of organisms related to
 CC C. glutamicum, identify and localise C. glutamicum sequences of interest,
 CC in evolutionary studies, in determining SMP protein sequences required
 CC for function, in modulating SMP protein activity, in modulating the
 CC metabolism of sugars, and in modulating high-energy molecule production
 CC in a cell (i.e. ATP, NADPH).
 CC
 XX
 SO Sequence 1860 BP; 426 A; 405 C; 562 G; 467 T; 0 other;
 Query Match 86.1%; Score 1860; DB 22; Length 1860;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1860; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 361 GCATCGAATAGTGTGCGAAGGTGTTGGCCATCGCTAGCCATATTCCAGATGCCCAAGATTGG 420
 QY 647 TTGACGTTCTTCAGAGAAACGATCCGAGATTTTAAAGAAATGCTGTGTTACTG 706
 Db 421 TTGACGTTCTTCAGAGAAACGATCCGAGATTTTAAAGAAATGCTGTGTTACTG 480
 QY 707 CGAGATGTGAATGTGTGTAGCAAGGTGTAACGCAATTTTGCATACCCGATTCAGTCAC 766
 Db 481 CGAGATGTGAATGTGTGTAGCAAGGTGTAACGCAATTTTGCATACCCGATTCAGTCAC 540
 QY 767 CATGGCGGGTAAAGGTGTGTGCGTAGTAGATTCGCGATATTCGCTAAAGAAAGCC 826
 Db 541 CATGGCGGGTAAAGGTGTGTGCGTAGTAGATTCGCGATATTCGCTAAAGAAAGCC 600
 QY 827 AGGTGACGTTACTTATTCATATTCACATTTCTTTCGACATCTGTGTGTCCCGGA 886
 Db 601 AGGTGACGTTACTTATTCACATTTCTTTCGACATCTGTGTGTCCCGGA 660
 QY 887 TCCTACTGAGGCTGACAGCGCTGTGTGAGGCGATTAACACGCTAAGTCTGACTTTGTT 946
 Db 661 TCCTACTGAGGCTGACAGCGCTGTGTGAGGCGATTAACACGCTAAGTCTGACTTTGTT 720
 QY 947 CTCGGGTGCGGGGTGAAGAATGCTGCGCGCAAGTGTGAGAGTTGGCGGAGAGATTAA 1006
 Db 721 CTCGGGTGCGGGGTGAAGAATGCTGCGCGCAAGTGTGAGAGTTGGCGGAGAGATTAA 780
 QY 1007 ATCACCAGATGGGCATGCGCTGTGTGTGAAGCAGTACATCAGCATAGATCCGTTGA 1066
 Db 781 ATCACCAGATGGGCATGCGCTGTGTGTGAAGCAGTACATCAGCATAGATCCGTTGA 840
 QY 1067 GGTGCGCATATCTGCGCTGCTGTGTGTGAAGCAGTACATCAGCATAGATCCGTTGA 1126
 Db 841 GGTGCGCATATCTGCGCTGCTGTGTGTGAAGCAGTACATCAGCATAGATCCGTTGA 900
 QY 1127 TCTGCTGATCTTATTTGGGTACGATTTCCCTTATTCGATTTCCCTTAAAGCAACGT 1186
 Db 901 TCTGCTGATCTTATTTGGGTACGATTTCCCTTATTCGATTTCCCTTAAAGCAACGT 960
 QY 1187 TGCCCAAGTGTGATATACAGCGTGCACATTTGTCGACATACAGCGGTGAAGTATCCGT 1246
 Db 961 TGCCCAAGTGTGATATACAGCGTGCACATTTGTCGACATACAGCGGTGAAGTATCCGT 1200
 QY 1247 GACCGGTGATGTTGCTGCAACAATGCAAAATATTTTGCCTCATGTGAAGAAACACA 1306
 Db 1021 GACCGGTGATGTTGCTGCAACAATGCAAAATATTTTGCCTCATGTGAAGAAACACA 1080
 QY 1307 TCGTTCCTTCCTTGATCGGATGCTCAAGGCACAGACGCTAAGTGAAGCTCGGTGTAGA 1366
 Db 1081 TCGTTCCTTCCTTGATCGGATGCTCAAGGCACAGACGCTAAGTGAAGCTCGGTGTAGA 1140
 QY 1367 GACGTTACACATTAACGTGAGAGCATGTGCTATTTCACCTGAATACGTTGCTCTAT 1426
 Db 1141 GACGTTACACATTAACGTGAGAGCATGTGCTATTTCACCTGAATACGTTGCTCTAT 1200
 QY 1427 TTTGAACGAGTGGCGGATTAAGATGCGGTGTTTACTGTGAGTACCGGATGTGCAATGT 1486
 Db 1201 TTTGAACGAGTGGCGGATTAAGATGCGGTGTTTACTGTGAGTACCGGATGTGCAATGT 1260
 QY 1487 GTGCGATGCGAGGTACATCGAGATTCGAGAGGAAACGCGCATTTGTGGTTCAATCCG 1546
 Db 1261 GTGCGATGCGAGGTACATCGAGATTCGAGAGGAAACGCGCATTTGTGGTTCAATCCG 1320
 QY 1547 CCACGGCACAGATGGCTAATGCTTGCTTCATGCGAATGTGTGCGCAAAAGTGTGATGANA 1606
 Db 1321 CCACGGCACAGATGGCTAATGCTTGCTTCATGCGAATGTGTGCGCAAAAGTGTGATGANA 1380
 QY 1607 CCGCAGGTGATCGGATGTGTGCGGATGAGTGTGTTGGCAAGTGTGCGGAGTGTCT 1666
 Db 1381 CCGCAGGTGATCGGATGTGTGCGGATGAGTGTGTTGGCAAGTGTGCGGAGTGTCT 1440
 QY 1667 GACCGTTAAGCTGACCAACTTCGCTGAAGGCTGTGTTTAAACAACAGTCTTTGGG 1726
 Db 1441 GACCGTTAAGCTGACCAACTTCGCTGAAGGCTGTGTTTAAACAACAGTCTTTGGG 1500

QY 1727 CATGSGAAGTTGGAGATGCTGCTGGAGGAGACAGCCAGATTGGTACTGACCATGAGGA 1786
 DB 1501 CATGSGAAGTTGGAGATGCTGCTGGAGGAGACAGCCAGATTGGTACTGACCATGAGGA 1560
 QY 1787 AGTGAATTTGCGAGATTTGGCGGCTGCGGCTATCAAAATCGGTACGACATCAGGATCC 1846
 DB 1561 AGTGAATTTGCGAGATTTGGCGGCTGCGGCTATCAAAATCGGTACGACATCAGGATCC 1620
 QY 1847 GAGAAAGTTGGCGAGGAGCTAGCTGAGGACATTTGCTGAGCTGCTGATGATGCA 1906
 DB 1621 GAGAAAGTTGGCGAGGAGCTAGCTGAGGACATTTGCTGAGCTGCTGATGATGCA 1680
 QY 1907 TATGCTCAGGATGCTTAAATGCGCTGATCCACCAACCATCACTGAGGAGGATCAT 1966
 DB 1681 TATGCTCAGGATGCTTAAATGCGCTGATCCACCAACCATCACTGAGGAGGATCAT 1740
 QY 1967 GGGATTTGAGCAAGCGGCGCCACCCGACCGTCTTTGGTGGAGAGTAGAGCGATGATGA 2026
 DB 1741 GGGATTTGAGCAAGCGGCGCCACCCGACCGTCTTTGGTGGAGAGTAGAGCGATGATGA 1800
 QY 2027 TCTGGCCGTTGAGCATAGGATATCTCTACTGATGATGATGATGATGATGATGATGAT 2086
 DB 1801 TCTGGCCGTTGAGCATAGGATATCTCTACTGATGATGATGATGATGATGATGATGAT 1860
 RESULT 9
 AAH67838
 ID AAH67838 standard: DNA: 1737 BP.
 XX AAH67838:
 AC
 XX 26-SEP-2001 (first entry)
 DT
 XX
 DE C glutamicum coding sequence fragment SEQ ID NO: 2873.
 XX
 KW Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
 KM organic acid synthesis; ds.
 XX
 OS Corynebacterium glutamicum.
 PN
 PD EPI108790-A2.
 XX 20-JUN-2001.
 PE 18-DEC-2000: 2000EP-0127688.
 XX
 PR 16-DEC-1999: 99JP-0377484.
 PR 07-APR-2000: 2000JP-0159162.
 PR 03-AUG-2000: 2000JP-0280988.
 XX
 PA (KYO) KYOWA HAKKO KOGYO KK.
 PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
 PI Tateishi N, Senoh A, Ikeda M, Ozaki A;
 DR WPI: 2001-376931/40.
 DR P-PDB: AAG92619.
 XX
 PT Novel polynucleotides derived from Coryneform bacteria, for identifying
 PT mutation point of a gene, measuring expression of a gene, analysing
 PT expression profile or pattern of a gene and identifying homologous gene
 PT
 PS Claim 8: SEQ ID NO: 2873; 246pp + Sequence Listing: English.
 XX
 CC The present invention provides a number of nucleotide and protein
 CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These
 CC are useful for identifying the mutation point of a gene derived from a
 CC mutant of coryneform bacterium, measuring expression amount and
 CC analysing the expression profile or expression pattern of a gene derived
 CC from Coryneform bacterium, and identifying a homologue of a gene derived
 CC from coryneform bacterium. Coryneform bacteria are useful for producing

CC amino acids, nucleic acids, vitamins, saccharides and organic acids,
 CC particularly L-lysine. The present sequence is a nucleic acid described
 CC in the exemplification of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from the
 CC European Patent Office.
 XX
 SQ Sequence 1737 BP; 388 A; 380 C; 528 G; 441 T; 0 other;
 Query Match 80.4%; Score 1737; DB 22; Length 1737;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1737; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 327 ATGCGACACAGCTACGAGAAATTAATGACACTTGGACGCTCAAGGTGTAACCGA 386
 DB 1 ATGCGACACAGCTACGAGAAATTAATGACACTTGGACGCTCAAGGTGTAACCGA 60
 QY 387 ATTTATGTTGGTGGGTGACAGGCTTAATCCAGTCGTGATGCTGCCCAATCAGAT 446
 DB 61 ATTTATGTTGGTGGGTGACAGGCTTAATCCAGTCGTGATGCTGCCCAATCAGAT 120
 QY 447 ATTAGAGTGGTGCACGTTCCGAATAGAGAGGCGGCGCTTTCAGCGGAGTGGGATCG 506
 DB 121 ATTAGAGTGGTGCACGTTCCGAATAGAGAGGCGGCGCTTTCAGCGGAGTGGGATCG 180
 QY 507 TTGATCACTGGGAGCTGGCAGATATGCTGCTCTTGTGGTCTGGAACACACACTG 566
 DB 181 TTGATCACTGGGAGCTGGCAGATATGCTGCTCTTGTGGTCTGGAACACACACTG 240
 QY 567 ATTGAGGCTCTTATGATTCGATCGCAAAATGTCGCAAGGTGTTGGCCATCGTACCAT 626
 DB 241 ATTGAGGCTCTTATGATTCGATCGCAAAATGTCGCAAGGTGTTGGCCATCGTACCAT 300
 QY 627 ATTCGAGTGGCCGATGTTGTTGACGCTTCTCCAGAAACGATCCGAGATTTGTT 686
 DB 301 ATTCGAGTGGCCGATGTTGTTGACGCTTCTCCAGAAACGATCCGAGATTTGTT 360
 QY 687 AAGGAATGCTGTGTTACTGCGAGATGTCGATGTCGACAGGTGACGATTTTG 746
 DB 361 AAGGAATGCTGTGTTACTGCGAGATGTCGATGTCGACAGGTGACGATTTTG 420
 QY 747 CATCAGCGATTTGATGCTCACCACATGGCGGATTAAGGTGTCGATGATTCGCGT 806
 DB 421 CATCAGCGATTTGATGCTCACCACATGGCGGATTAAGGTGTCGATGATTCGCGT 480
 QY 807 GATATCGCTAAGAAAGCAGGTGACGATCTTATTCCAATTCCTATTTCTGCG 866
 DB 481 GATATCGCTAAGAAAGCAGGTGACGATCTTATTCCAATTCCTATTTCTGCG 540
 QY 867 ACTCGTGGTGTCCCGGATCCATGAGGCTGCGAGCGGTGGAGGAGGATTAACAC 926
 DB 541 ACTCGTGGTGTCCCGGATCCATGAGGCTGCGAGCGGTGGAGGAGGATTAACAC 600
 QY 927 GCTAAGTCTGACATTTGTTCTGCGGTGCGGCGTGAAGATGCTCCGCGCAGGTG 986
 DB 601 GCTAAGTCTGACATTTGTTCTGCGGTGCGGCGTGAAGATGCTCCGCGCAGGTG 660
 QY 987 GAGTTGGCGGAGAAATTAATTCACCATGCGGATCGCGGTGGTAAACATACATC 1046
 DB 661 GAGTTGGCGGAGAAATTAATTCACCATGCGGATCGCGGTGGTAAACATACATC 720
 QY 1047 CAGCATGAGATTCGTTGAGTGGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1106
 DB 721 CAGCATGAGATTCGTTGAGTGGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
 QY 1107 GATGCGTCAATGAGCGGATCTCTGATTTATTTGATGATGATTTCTTATTCGAT 1166
 DB 781 GATGCGTCAATGAGCGGATCTCTGATTTATTTGATGATGATTTCTTATTCGAT 840
 QY 1167 TTCTTCTTAAGCAACGTTGCCAGTGGATTCACAGGTTGGCGCATTTGGTGGAGCT 1226
 DB 841 TTCTTCTTAAGCAACGTTGCCAGTGGATTCACAGGTTGGCGCATTTGGTGGAGCT 900

QY 1227 ACCACGGTGAAGTATCCGGTACCGGATGATGTTGTCACAACTCGAAAATATTTGGCT 1286
 DB 901 ACCACGGTGAAGTATCCGGTACCGGATGATGTTGTCACAACTCGAAAATATTTGGCT 960
 QY 1287 CATGTGAAGAAAAAACAAGTCTGCTCTTCTTGATCGATGCTCAAGCAGCAGCGT 1346
 DB 961 CATGTGAAGAAAAAACAAGTCTGCTCTTCTTGATCGATGCTCAAGCAGCAGCGT 1020
 QY 1347 AAGTGAAGCTGGTGTAGAGAGCTACACATACGTCAGAGATGTCCTATTTCAC 1406
 DB 1021 AAGTGAAGCTGGTGTAGAGAGCTACACATACGTCAGAGATGTCCTATTTCAC 1080
 QY 1407 CCTGAATACGTTGCTCTTATTTTGAACAGCTGGCGAATAGAGATGCTTTACTGTC 1466
 DB 1081 CCTGAATACGTTGCTCTTATTTTGAACAGCTGGCGAATAGAGATGCTTTACTGTC 1140
 QY 1467 GATACGGGATGTCATGTCGATGTCGATGTCGATGTCGATGTCGATGTCGATGTC 1526
 DB 1141 GATACGGGATGTCATGTCGATGTCGATGTCGATGTCGATGTCGATGTCGATGTC 1200
 QY 1527 GACTTTGTGGTTCATTCGCCACAGCGATGCTAATGCTTGGCTATGCGATTGCT 1586
 DB 1201 GACTTTGTGGTTCATTCGCCACAGCGATGCTAATGCTTGGCTATGCGATTGCT 1260
 QY 1587 GCGCAAGTGTGATGTCGAAACCCGACGATGCTGATGCTGATGCTGATGCTGATG 1646
 DB 1261 GCGCAAGTGTGATGTCGAAACCCGACGATGCTGATGCTGATGCTGATGCTGATG 1320
 QY 1647 ATGCTGCTGGTGAAGTCTTGCACCGCTTAAGCTGACACCACTTCCGCTGAAGGCTGCTG 1706
 DB 1321 ATGCTGCTGGTGAAGTCTTGCACCGCTTAAGCTGACACCACTTCCGCTGAAGGCTGCTG 1380
 QY 1707 TTTTAAACAAGTCTTGGGCGATGTCGATGTCGATGTCGATGTCGATGTCGATGTC 1766
 DB 1381 TTTTAAACAAGTCTTGGGCGATGTCGATGTCGATGTCGATGTCGATGTCGATGTC 1440
 QY 1767 TTTGCTAGTACGATGTCGATGTCGATGTCGATGTCGATGTCGATGTCGATGTC 1826
 DB 1441 TTTGCTAGTACGATGTCGATGTCGATGTCGATGTCGATGTCGATGTCGATGTC 1500
 QY 1827 TCGGTACGATGTCGATGTCGATGTCGATGTCGATGTCGATGTCGATGTCGATGTC 1886
 DB 1501 TCGGTACGATGTCGATGTCGATGTCGATGTCGATGTCGATGTCGATGTCGATGTC 1560
 QY 1887 CCTGACCTGATGTCGATGTCGATGTCGATGTCGATGTCGATGTCGATGTCGATGTC 1946
 DB 1561 CCTGACCTGATGTCGATGTCGATGTCGATGTCGATGTCGATGTCGATGTCGATGTC 1620
 QY 1947 ATCAGTGGGAAACGATGTCGATGTCGATGTCGATGTCGATGTCGATGTCGATGTC 2006
 DB 1621 ATCAGTGGGAAACGATGTCGATGTCGATGTCGATGTCGATGTCGATGTCGATGTC 1680
 QY 2007 GGAAGTAGAGATGTCGATGTCGATGTCGATGTCGATGTCGATGTCGATGTCGATGTC 2063
 DB 1681 GGAAGTAGAGATGTCGATGTCGATGTCGATGTCGATGTCGATGTCGATGTCGATGTC 1737

RESULT 10
 AAF71404
 ID AAF71404 standard; DNA; 944 BP.
 XX AAF71404;
 AC
 XX 30-APR-2001 (first entry)
 DE Corynebacterium glutamicum SMP protein nucleotide sequence SEQ ID NO: 89.
 XX
 XX Corynebacterium glutamicum; carbon metabolism and energy production;
 KW SMP protein; sugar metabolism and oxidative phosphorylation protein;
 KW fine chemical production; organic acid; proteinogenic amino acid;
 KW nonproteinogenic amino acid; putine base; pyrimidine base; nucleoside;
 KW nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol;
 KW carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme;

KW diagnosis; Corynebacterium diphtheriae; evolutionary study; ds.
 XX
 OS Corynebacterium glutamicum.
 XX
 PN W0200100844-A2.
 PD 04-JAN-2001.
 XX
 PF 23-JUN-2000; 2000MO-1B00943.
 PR 25-JUN-1999; 99US-0141031.
 PR 08-JUL-1999; 99DE-1031412.
 PR 08-JUL-1999; 99DE-1031413.
 PR 08-JUL-1999; 99DE-1031419.
 PR 08-JUL-1999; 99DE-1031420.
 PR 08-JUL-1999; 99DE-1031424.
 PR 08-JUL-1999; 99DE-1031428.
 PR 08-JUL-1999; 99DE-1031431.
 PR 08-JUL-1999; 99DE-1031434.
 PR 08-JUL-1999; 99DE-1031510.
 PR 08-JUL-1999; 99DE-1031562.
 PR 08-JUL-1999; 99DE-1031634.
 PR 09-JUL-1999; 99DE-1032180.
 PR 09-JUL-1999; 99DE-1032227.
 PR 09-JUL-1999; 99DE-1032230.
 PR 09-JUL-1999; 99US-0143208.
 PR 14-JUL-1999; 99DE-1032924.
 PR 14-JUL-1999; 99DE-1032973.
 PR 14-JUL-1999; 99DE-1033005.
 PR 27-AUG-1999; 99DE-1040765.
 PR 31-AUG-1999; 99US-0151572.
 PR 03-SEP-1999; 99DE-1042076.
 PR 03-SEP-1999; 99DE-1042079.
 PR 03-SEP-1999; 99DE-1042086.
 PR 03-SEP-1999; 99DE-1042087.
 PR 03-SEP-1999; 99DE-1042088.
 PR 03-SEP-1999; 99DE-1042095.
 PR 03-SEP-1999; 99DE-1042123.
 PR 03-SEP-1999; 99DE-1042125.
 XX
 PA (BADI) BASF AG.
 XX
 PI Pompejus M, Kroegeer B, Schroeder H, Zelder O, Haberhauer G;
 DR MPI: 2001-061975/07.
 DR P-PSDB: AAB79287.
 XX
 PT New isolated Corynebacterium glutamicum nucleic acid encoding a sugar
 PT metabolism and oxidative phosphorylation protein for production or
 PT modulation of production of fine chemicals e.g. amino acids,
 PT carbohydrates or enzymes -
 XX
 PS Claim 3; Page 274-275; 1246pp; English.
 CC AAF71360 to AAF71750 encode the Corynebacterium glutamicum sugar
 CC metabolism and oxidative phosphorylation (SMP) proteins given in
 CC AAB79243 to AAB 79633 which are involved in carbon metabolism and
 CC energy production. The C. glutamicum SMP gene can be used in vectors
 CC (II) for expression in host cells and production or modulation of
 CC production of fine chemicals, such as, an organic acid, a proteinogenic
 CC or nonproteinogenic amino acid (preferred), a purine or pyrimidine base,
 CC a nucleoside, a nucleotide, a lipid, a saturated or unsaturated fatty
 CC acid, a diol, a carbohydrate, an aromatic compound, a vitamin, a
 CC cofactor, a polyketide, or an enzyme. The presence of (I) or SMP proteins
 CC (III) encoded by them are used for diagnosing the presence or activity of
 CC Corynebacterium diphtheriae in a subject. (I), (II), (III) or host cells
 CC containing them are used to map genomes of organisms related to
 CC C. glutamicum, identify and localise C. glutamicum sequences of interest,
 CC in evolutionary studies, in determining SMP protein regions required
 CC for function, in modulating SMP protein activity, in modulating the
 CC metabolism of sugars, and in modulating high-energy molecule production
 CC in a cell (i.e. ATP, NADPH).

RESULT 11

181 GATCCCTACCTGAGGCGTGGTGGAGGCGATTACCAACGCTAAGTCGTCACTTTC 240

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Db      241 TTCTGGCGTGGGGCGCTGGAAGATGCTCGCGCCAGCTTTGGAGTTGGCGGAGAGATT
QY      1005 AAATACCGATCGCGGATGCGCTGGTGGTACAGTACATCCAGCATAGAAATCCGTTT
Db      301 AAATACCGATCGCGGATGCGCTGGTGGTACAGTACATCCAGCATAGAAATCCGTTT
QY      1065 GAGGTGGGATGTTGGCCCTGTTGGTACGGCGCTGGTGGTACAGTACATCCAGCATAGAAATCCGTTT
Db      361 GAGGTGGGATGTTGGCCCTGTTGGTACGGCGCTGGTGGTACAGTACATCCAGCATAGAAATCCGTTT
QY      1125 GATCTGCTGATTTATTTGGTACGATTTCCCTATTTGATTTCTTCTTAAGACAAC
Db      421 GATCTGCTGATTTATTTGGTACGATTTCCCTATTTGATTTCTTCTTAAGACAAC
QY      1185 GTTCCCGAGGTGATATCAAGGTGGGACATTTGTCGACGATCCAGGTGAGATCCG
Db      481 GTTCCCGAGGTGATATCAAGGTGGGACATTTGTCGACGATCCAGGTGAGATCCG
QY      1245 GTGACCGGATGTTGCTGCAACATCGAAATATTTTGCCTATGTGAAGAAAAACA
Db      541 GTGACCGGATGTTGCTGCAACATCGAAATATTTTGCCTATGTGAAGAAAAACA
QY      1305 GATCTGCTGCTCTGATGATGCGATGCTCAAGGACAGGATGATGAGTGGTGGTGA
Db      601 GATCTGCTGCTCTGATGATGCGATGCTCAAGGACAGGATGATGAGTGGTGGTGA
QY      1365 GAGACGTACACATTAACGTCGAGACATGTCCTATTACCTGATATCGTTGCCCTCT
Db      841 CGCCACGGACGATGGCTTAATGGCTTCCCTCATGCG 875

RESULT 12
AAD20204
ID      AAD20204 standard; DNA; 875 BP.
AC      AAD20204;
DT      03-JAN-2002 (first entry)
XX      PCR product of C. glutamicum poxB internal fragment DNA.
DE      L-amino acid; fermentation; coryneform bacteria; animal nutrition;
KW      glucose 6-phosphate dehydrogenase; zwf; human medicine;
KM      foodstuff industry; pyruvate oxidase; poxB;
NM      pharmaceutical industry; ds.
OS      Corynebacterium glutamicum.
PN      WO200170995-A1.
XX      27-SEP-2001.
PD      05-JUL-2000; 2000WO-EP06303.
PE      20-MAR-2000; 2000US-0531269.
PR      (DEGS) DEGUSSA AG.
PA      (KERJ) FORSCHUNGSZENTRUM JUELICH GMBH.
PA      (UYNA-) UNIV NAT IRELAND.
XX

```

```

PI      Burke K, Sahn H, Eggeling L, Moritz B, Dunican LK, McCormack A;
PI      Stempelton C, Moeckel B, Thierbach G;
XX      WPI: 2001-639130/73.
DR      1005
XX      301
XX      1065
XX      361
XX      1125
XX      421
XX      1185
XX      481
XX      1245
XX      541
XX      1305
XX      601
XX      1365
XX      841

Query Match
Best Local Similarity 100.0%; Pred. No. 7.7e-269; Length 875;
Matches 875; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 875 BP; 190 A; 193 C; 266 G; 226 T; 0 other;

Example 10: Page 59-60; 63pp; English.

The present invention relates to a method for preparing L-amino acids by
fermenting coryneform bacteria, comprising fermenting the L-amino acid
producing bacteria in which at least the glucose 6-phosphate
dehydrogenase (zwf) gene is amplified, and concentrating and isolating
the L-amino acid produced. The L-amino acids produced are used in animal
nutrition, human medicine, foodstuffs industry and the pharmaceuticals
industry. The present sequence is the PCR product of
Corynebacterium glutamicum strain AS019 pyruvate oxidase (poxB) internal
fragment DNA.

```


GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 3, 2003, 15:09:07 : Search time 7709 Seconds

(without alignments)
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Title: US-09-965-825-1

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Searched: 288711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 100%

Listing first 45 summaries

Database :

GenBank:
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2: gb.htg:*
3: gb.in:*
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6: gb.pat:*
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8: gb.pl:*
9: gb.pr:*
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11: gb.sts:*
12: gb.sy:*
13: gb.un:*
14: gb.vi:*
15: em.ba:*
16: em.fun:*
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35: em.htg.rod:*
36: em.htg.mam:*
37: em.htg.vrt:*
38: em.sy:*
39: em.htgo.hum:*
40: em.htgo.mus:*
41: em.htgo.other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	2160	100.0	2160	AX137665	AX137665 Sequence
2	2160	100.0	2160	AX250315	AX250315 Sequence
3	2160	100.0	2160	AX253245	AX253245 Sequence
4	2160	100.0	2160	AX253251	AX253251 Sequence
5	2160	100.0	2160	AX404607	AX404607 Sequence
6	2160	100.0	2160	BD014868	BD014868 Novel nuc
7	2160	100.0	3248	AX404610	AX404610 Sequence
8	2160	100.0	320550	AP005282	AP005282 Coryneb
9	2160	100.0	349980	AX127152	AX127152 Sequence
10	1860	86.1	1860	AX064959	AX064959 Sequence
11	1737	80.4	1737	AX122957	AX122957 Sequence
12	1737	80.4	1737	BD165074	BD165074 Novel pol
13	944	43.7	944	AX064963	AX064963 Sequence
14	875	40.5	875	AX137667	AX137667 Sequence
15	875	40.5	875	AX250317	AX250317 Sequence
16	875	40.5	875	AX253247	AX253247 Sequence
17	875	40.5	875	AX253253	AX253253 Sequence
18	875	40.5	875	AX404609	AX404609 Sequence
19	875	40.5	875	BD014869	BD014869 Novel nuc
20	551	25.5	552	AX064961	AX064961 Sequence
21	532.4	24.6	295150	SC0939126	SC0939126 Streptomy
22	523	24.2	298550	AP005029	AP005029 Streptomy
23	394.8	18.3	13074	AE012116	AE012116 Xanthomon
24	393.2	18.2	298550	AP005961	AP005961 Bradyrhiz
25	381.8	17.7	310325	AE016864	AE016864 Pseudomon
26	377.2	17.5	11312	AE011647	AE011647 Xanthomon
27	352.4	16.3	10795	AE013885	AE013885 Yersinia
28	352.4	16.3	199050	AE015111	AE015111 Shigella
29	346.2	16.0	294050	AE014147	AE014147 Yersinia
30	346.2	16.0	301983	AE016840	AE016840 Salmonell
31	345	16.0	65219	AE008737	AE008737 Salmone
32	338.8	15.7	297816	AP002553	AP002553 Escherich
33	338.4	15.7	10658	AE005268	AE005268 Escherich
34	337.2	15.6	8973	AV081837	AV081837 Bradyrhiz
35	329.2	15.2	10516	AE015111	AE015111 Shigella
36	329.2	15.2	290029	AE016980	AE016980 Shigella
37	324.4	15.0	1422	AX404618	AX404618 Sequence
38	321.2	14.9	301276	AE016758	AE016758 Escherich
39	305.2	14.1	1719	AX469493	AX469493 Sequence
40	305.2	14.1	1974	ECPOXB	ECPOXB
41	305.2	14.1	11429	AE000188	AE000188 Escherich
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44	302	14.0	1719	ECPOXB	ECPOXB
45	302	14.0	1719	ECPOXB10G	ECPOXB10G

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE
AX137665	AX137665	Sequence 1 from Patent EP1096013.	AX137665	AX137665	GI:14273850	Corynebacterium glutamicum	Corynebacterium glutamicum	1	Meckel,B., Weissenborn,A., Pfeifferle,W., Puehler,A., Kallinowski,J., Bache,B. and Dusch,N.	Nucleotide sequence encoding corynebacterium poxb-gene and its use

JOURNAL In the preparation of L-lysine
Patent: EP 1096013-A 1 02-MAY-2001;
Degussa AG (DE)

FEATURES
Location/Qualifiers
1. 2160

/organism="Corynebacterium glutamicum"

/mol_type="genomic DNA"

/db_xref="taxon:11718"

-35_signal 227..232

-10_signal 256..261

CDS 327..2066

/note="unnamed protein product"

/codon_start=1

/transl_table=11

/protein_id="CAC39916.1"

/db_xref="GI:14273851"

/translation="MAHSAEOLIDLEAGYKRIYGLVDSINPVDVRODIEKV
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SAOIGSTFEDETHPELIRKESCTCEMNGEGERILHIAIOTMAGKGVSVVPIG
DIKEDGDSITNSSTISSGTVEPEPDEALVALEAINNASVILECGAVKMAAO
VLELAERKISPIHALGKQYIOHNPFEVMSGLIGYACVADNEADLILGLTDF
PYSDFLPKDNVAQVDINGAHIGRTITVKPVGDVAATLLENILPHKERTDSFLDM
LKAHERKLSVETVTHNVEKHVPIPEVVASILNELADKDAVETVDMCMVMHARY
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Dd		1981	CGGCCACCCGAACCGTCTTGTGGTGGAGAGTAGGAGCGATGATGATCTGGCCCCGTTGGA	2040
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Dd		2041	ACATAAGGAATATATCTACTCCATGATGATGATGATGATGATACACCTGCTGTCTCATGACCGCGA	2100
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VERSION		AXZ50315.1	GI:15984083	
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REFERENCE		1	Dunican,L.K., Stapelton,C., Burke,K., Moeckel,B. and Thierbach,G. Process for the fermentative preparation of L-amino acids with amplification of the tkt gene Patent: WO 0168894-A 3 20-SEP-2001;	
AUTHORS			Debusa AG (DE) ; National University of Ireland (IE)	
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BASE COUNT		491 a	486 c	647 g 536 t

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RESULT 3
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LOCUS
DEFINITION
ACCESSION
VERSION
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Corynebacterium glutamicum
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Bacteria; Actinobacteria; Actinobacteriales; Corynebacteriales; Corynebacterium.

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BASE COUNT
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Query Match
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DEFINITION Sequence 4 from Patent WO0170995.
ACCESSION AX253251
VERSION AX253251.1 GI:16073799
KEYWORDS
SOURCE
ORGANISM
Corynebacterium glutamicum
Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.
REFERENCE
1 Burke, K., Sahm, H., Eggeling, L., Moritz, B., Dunican, L.K.,
Stapelton, C., Moeckel, B. and Thierbach, G.
Processes for the fermentative preparation of L-amino acids with
amplification of the zwf gene
Patent: WO 0170995-A 4 27-SEP-2001;
Degussa AG (DE) ; FORSCHUNGSZENTRUM JUELICH GMBH (DE) ; National
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LOCUS BD014868 2160 bp DNA linear PAT 27-AUG-2002
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 ACCESSION BD014868
 VERSION BD014868.1 GI:22555675
 KEYWORDS JP 2001161386-A/1.
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 ORGANISM Corynebacterium glutamicum
 Bacteria; Actinobacteria; Actinobacteriales; Corynebacteriaceae; Corynebacterium.
 REFERENCE
 AUTHORS Doush, N., Baate, B., Kalinowski, J., Alfred, Puehler, Meckel, V., Weisenborn, A. and Pfeifferle, W.
 TITLE Novel nucleotide sequence encoding poxb-gene
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 PR 28-OCT-1999 DE 19951975.7
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 PC ANKE WEISENBORN, WALTER PFEFFERLE
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 DEFINITION Sequence 4 from Patent WO0229020.
 ACCESSION AX404610
 VERSION AX404610.1 GI:21437891
 KEYWORDS
 SOURCE
 ORGANISM
 Corynebacterium glutamicum
 Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;
 Corynebacteriaceae; Corynebacterium.
 REFERENCE
 1 Dusch, N., Herrmann, T. and Thierbach, G.
 Process for the fermentative preparation of D-pantothenic acid
 using Corynebacterium bacteria
 Patent: WO 0229020-A 4 11-Apr-2002;
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 1 Nakagawa, S., Mizoguchi, H., Ando, S., Hayashi, M., Ochiai, K.,
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 Novel polynucleotides
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DEFINITION      Sequence 85 from Patent WO0100844.
ACCESSION      AX064959
VERSION        AX064959.1  GI:12542671
KEYWORDS
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REFERENCE
  1  Pompeius M., Kroeger B., Schroeder H., Zelder O. and Haberhauer G.
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RESULT 11
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 ACCESSION AX122957
 VERSION AX122957.1 GI:14040445
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 NAKAGAWA, S., MIZOGUCHI, H., ANDO, S., HAYASHI, M., OCHIAI, K.,
 YOKOI, H., TATEISHI, N., SENOH, A., IKEDA, M. and OZAKI, A.,
 Novel polynucleotides
 Patent: EP 1108790-A 2873-20-JUN-2001;
 KIOKA HAKKO KOGYO CO., LTD. (JP)


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PD 09-JUL-2002
PF 15-DEC-2000 JP 2000405096
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PI HARUHIKO YOKOI, NAKO TATEISHI, AKIHIRO SENOO, MASATO IKEDA, AKIO
PI OZAKI
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 REFERENCES
 1 Dunican, L.K., Stapleton, C., Burke, K., Moeckel, B. and Phierbach, G.
 Process for the fermentative preparation of L-amino acids with
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 Patent: WO 0168894-A 5 20-SEP-2001;
 Degussa AG (DE); National University of Ireland (IE)
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 Db 781 GTGTGCGATGCGAGTACATCGAGATCCGAGGGAAGCGGCACTTTGTGGTTCAATC 840
 QY 1545 CGCCACGGCAGATGGCTAATGCGTTCCTCATGC 1579
 Db 841 CGCCACGGCAGATGGCTAATGCGTTCCTCATGC 875

Search completed: October 3, 2003, 17:41:27

Tue Oct 7 07:11:10 2003

us-09-965-825-1.rge

Page 20

Job time : 7717 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 3, 2003, 15:10:07 : Search time 4096 Seconds

(without alignments)
12816.814 Million cell updates/sec

Title: US-09-965-825-1

Perfect score: 2160

Sequence: 1 ttagagcgcgtctctgtgag.....gttgcacatgagatgcct 2160

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 22781392 segs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

```

1: em_estba:*
2: em_estbm:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_est3:*
12: gb_est4:*
13: gb_est5:*
14: gb_est6:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vit:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vil:*
28: gb_gss1:*
29: gb_gss2:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	183	8.5	601	BH010685	BH010685 ep67h04.g
2	150.2	7.0	906	CNS0104W	AL153073 Anopheles
3	109	5.0	1451	B2571467	B2571467 msh2.1902
4	105.8	4.9	487	CD288304	CD288304 3_p8.abd

5	104.8	4.9	731	29	CNS01PEV	AL141752 Anopheles
6	100.4	4.6	375	29	CNS0713Y	AL611872 Anopheles
7	100	4.6	837	29	B2571498	B2571498 msh2.1917
8	95.8	4.4	538	9	AM036130	AM036130 EST274506
9	91.6	4.2	1037	29	B2559326	B2559326 pac22.164
10	91.2	4.2	274	10	B6627542	B6627542 CC-est1cL
11	89.8	4.2	550	12	BM534496	BM534496 fwb9h06.y
12	87.4	4.0	769	29	B2549561	B2549561 pac31-60-
13	85.2	3.9	830	29	B2571612	B2571612 msh2.1969
14	72.2	3.3	299	28	BH241614	BH241614 AUL1B19TF
15	70.8	3.3	1862	28	BH708075	BH708075 LLMGtag61
16	69.8	3.2	467	9	AM036129	AM036129 EST274505
17	68	3.1	484	12	BM137811	BM137811 WHE0471-A
18	59.6	2.8	1202	29	B2579361	B2579361 msh2.6320
19	59.2	2.7	475	9	A1097766	A1097766 uc35f02.y
20	59.2	2.7	504	9	A1931656	A1931656 u171h04.y
21	59.2	2.7	561	4	BX516379	BX516379 RFPD Mus
22	59.2	2.7	577	10	BB638384	BB638384 BB638384
23	59.2	2.7	630	14	BY705708	BY705708 BY705708
24	59.2	2.7	701	10	BB653627	BB653627 BB653627
25	59.2	2.7	757	14	CB950802	CB950802 AGENCOURT
26	59.2	2.7	815	12	B1554388	B1554388 603235891
27	59.2	2.7	827	9	AU079796	AU079796 AU079796
28	59.2	2.7	918	12	B1690622	B1690622 603314217
29	59.2	2.7	1015	13	BQ960366	BQ960366 AGENCOURT
30	59.2	2.7	1974	11	AK005505	AK005505 Mus muscu
31	59.2	2.7	1976	11	AK050078	AK050078 Mus muscu
32	59.2	2.7	2615	11	AK041686	AK041686 Mus muscu
33	58	2.7	539	9	AW217660	AW217660 EST296374
34	58	2.7	639	10	BG130411	BG130411 EST476057
35	58	2.7	766	12	B1925329	B1925329 EST545218
36	58	2.7	770	12	B1935305	B1935305 EST555194
37	58	2.7	802	12	B1935831	B1935831 EST555720
38	57.6	2.7	845	10	BE282914	BE282914 601100571
39	57	2.6	593	9	AL865382	AL865382 AL865382
40	57	2.6	939	29	CNS01KC4	AL148149 Anopheles
41	55.8	2.6	335	13	BY141680	BY141680 BY141680
42	55.8	2.6	360	13	BY320483	BY320483 BY320483
43	55.8	2.6	362	13	BY147322	BY147322 BY147322
44	55.8	2.6	380	13	BY321497	BY321497 BY321497
45	55.8	2.6	430	14	CA544748	CA544748 K0103E03-

ALIGNMENTS

RESULT 1
BH010685
LOCUS
DEFINITION
ep67h04.g1 TO1000 Brassica oleracea genomic clone ep67h04 5',
genomic survey sequence.
ACCESSION
BH010685
VERSION
BH010685.1 GI:13956880
KEYWORDS
SOURCE
GSS.
ORGANISM
Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE
AUTHORS
Katari,M., O'Shaughnessy,A., Palmer,L., Bahret,A., Baker,J., Ballja
V., Bell,M., Cummins,D.M., King,L., Kirchoff,K., Kuit,K., Miller
B., Nascimento,L., Preston,R., Rodriguez,S., Santos,L., Shah,R.,
Vill.M.D., Zultavern,T., Bal,H., Dedhia,N. and McCombie,W.R.
Whole Genome Shotgun Reads from Brassica oleracea
Unpublished
Contact: W. Richard McCombie
Iltia Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org

TITLE
JOURNAL
COMMENT

Db 629 GAATTTGGCGGAAAGCTGAAA-CCCCGATGTGCTCCAGCCCTGCGGGCAAGAGACGCTC 687

QY 1047 CAGCATGAGAAATCCCTTTGAGTGGCGCATGTCTGGCCCTGTTGGTTACGGGCGCTGCTG 1106

Db 688 GAAATGAGTAACCCCTGACGATGATGAGCATGACCGGGGATGCGGTTTCTCCGGCTTC 747

QY 1107 GATGGCTCCAAATGAGCGGATCTGCTGATTTCTATGAGGTACGATTTCCCTTA--TTCT 1163

Db 748 CACACCATGATGAACGCCGACGACGCTGATBCTGCTGGGACCCACCATTTCCCTACCGCGC 807

QY 1164 GATTCCTCTCTTAAGAACAAGCTGGCCAGGTGATATCAACGGTGGCGACATTTGGTGA 1223

Db 808 TTATACCCGACGATGCTAAATCAATTCATTCATATCAACCCGACGATCGGCGCG 867

QY 1224 CGTACACGCTGAAGTATCCGCTGACCGGTGA 1255

Db 868 CACAGCAAGTGTGATATGCGCTGGTGGCGM 899

RESULT 3
BZ571467/c 1451 bp DNA linear GSS 17-DEC-2002

LOCUS msh2_1902.y2 msh Pseudomonas aeruginosa genomic clone msh2_1902.

DEFINITION

ACCESSION BZ571467

VERSION BZ571467.1 GI:27206528

KEYWORDS GSS.

SOURCE Pseudomonas aeruginosa

ORGANISM Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
1 (bases 1 to 1451)
Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M.,
Burns, J.L., Kaul, R. and Olsen, M.V.
Whole-Genome-Sequence Variation among Multiple Isolates of
Pseudomonas aeruginosa Library
J. Bacteriol., (2002) In press
Contact: Chris K. Raymond
Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 2066857244
Email: craymond@u.washington.edu
Class: Shotgun.
Location/Qualifiers

FEATURES
source 1..1451
/organism="Pseudomonas aeruginosa"
/mol_type="genomic DNA"
/strain="MSH"
/db_xref="taxon:287"
/clone="msh2_1902"
/clone_1lib="msh"
/note="Environmental isolate. Whole genomic shotgun
library."

BASE COUNT 271 a 358 c 394 g 263 t 165 others

ORIGIN

Query Match 5.0%; Score 109; DB 29; Length 1451;
Best Local Similarity 52.1%; Pred. No. 9.4e-20;
Matches 264; Conservative 0; Mismatches 242; Indels 1; Gaps 1;

QY 1447 AGGATCGGATGTTTCTGATACCGCATGTCGATGTCGATGCGAGGTACATCG 1506

Db 599 AGGAGCCCTGTTACACNNCGACGTCGCTGCGCATGTCTGCTGTTGGCTCACATC 540

QY 1507 AGAATCGGAGGAGGAGCGGCACTTGTGGGTTCAATCCGACGCGACGATGGCTAATG 1566

Db 539 CCTACACGCGGCAACGCTGTCACCTTCACAGCA-TGCTCCCGCGACCATATGGCGACG 481

QY 1567 CGTGGCTGATGCGGATTTGGTGGCAAGTGTGATGCAACCGCGCATGATCGGATGT 1626

Db 480 CCATGCCCAAGGCGCTGGGAGGAGGCTCTACTCCGAGCCCAAGTATCTCATCT 421

QY 1627 GTGGGATGTTGTTGGGATGCTGCTGGGTGAGCTTTGACCGCTTAAGTGTACCAAC 1686

Db 420 CCGGCGAGGGGCGCTGGCCATGCTGCTGGCGACCTGCTGACGCGCATCCAGGAAAAAC 361

QY 1687 TTCGCTGAAGGCTGTGTGTGTAAACAGATTCTTTGGCATGTGAGCTTGGAGATGC 1746

Db 360 TGCGGATCAACAGTATGTGTGTGAACATGCTGCTGGAACCTGTGAGCTGTGACACGA 301

QY 1747 TCGTGAAGGACAGCCAGATTTGTACTACCATGAGGAAGTAAATTTGCGACAGATTG 1806

Db 300 AGGTGAGAGGCGCTCTGACACACTACACCGACCTGCTCAACCCGACCTGCGCTTCG 241

QY 1807 CGGGGCGCTGGGATGATCAATTCGCTAGCATACCGATCGGAAGAAGTTGCGGACGAC 1866

Db 240 CCGAAGTATGCTGCTTCCACGACGCAAGGTGAGCGCTCCGAGAGCTCGAGCGGCGG 181

QY 1867 TAGCTGAGGCAATTTGGCATATCTGACCTGTACTGATGATATGTCACGGATCTAATG 1926

Db 180 TGCAAGATGTTCTGCGCCAGCCGCTGCTGGAGCTGCATACCAACCTTCGCG 121

QY 1927 CGCTGTGATCCCAACCATCATCAT 1953

Db 120 AGCTGTGATGCTGCGCGAAGATGAGT 94

RESULT 4
CD288304/c 487 bp mRNA linear EST 27-MAY-2003

LOCUS 3_P8.abd POE14_(Day_14_pregnant_ovine_endometrium) Ovis aries CDNA.

DEFINITION

ACCESSION CD288304

VERSION CD288304.1 GI:31086347

KEYWORDS EST.

SOURCE Ovis aries (sheep)

ORGANISM Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Caprinae; Ovis.
1 (bases 1 to 487)
Gray, C.A., Adelson, D.L. and Spencer, T.E.
Ovine ESTs
Unpublished
Contact: Thomas E. Spencer
Center for Animal Biotechnology and Genomics
Texas A&M University
Animal Science Dept., TAMU-2471, College Station, TX 77843-2471,
USA
Tel: 9798454896
Fax: 9798622862
Email: tspencer@ansc.tamu.edu.
Location/Qualifiers

FEATURES
source 1..487
/organism="Ovis aries"
/mol_type="mRNA"
/db_xref="taxon:9940"
/sex="female"
/tissue_type="endometrium"
/dev_stage="Day 14 pregnant"
/clone_1lib="POE14_(Day_14_pregnant_ovine_endometrium)"
/note="Organ: uterus; Vector: Triplex2; Site: 1; EcoRI;
Site 2: XhoI; Non-normalized library; sequenced 5' with
Triplex2 primer (CTCCGAGATCTGACGAGC). Library constructed
by Clontech with total RNA extracted using the Trizol
method and pooled from 5 females."

BASE COUNT 99 a 135 c 145 g 108 t

ORIGIN

Query Match 4.9%; Score 105.8; DB 14; Length 487;
Best Local Similarity 54.5%; Pred. No. 4.3e-19;
Matches 212; Conservative 0; Mismatches 177; Indels 0; Gaps 0;

[illegible]

QY	447	ATTGAGTGGGTGACGTTGCGAATGAGGAGGGGGTTTGACGCGGGCGGAATGC	508
Db	133	ATTGAATGGATGCCAGCCCGCATAGAGGTTGGCGTTTCCCGCGAGAT-NGNAACA	191
QY	507	TTGATCATTGGGAGCTGGCAGTATGCTGCTTTGTGTCCTGGAACAACACCTG	566
Db	192	CACCTTAGGGGAGTGGCGCTTCGCGCGGATCTCGGGCCGGGTAACCTGCACCTG	251
QY	567	ATTGACGGTCTTTATGATTTGCATCGAAATGCTGCCAAGTGTGGCCATGCGCAT	626
Db	252	ATCAACGGCCTTTTCAGCTGTACACGTAACCAACGTTCCGGTCTCGCATTTGCCGCCAC	311
QY	627	ATTCCGAGTGGCCAGTTGGTTGTCGACGTTCTTCAGGAAGCATCCGAGATTTTGT	686
Db	312	ATCCCTCTCTCGGAATCGCAGCGGCTATTTTCAGGAGACGACATCCGACA-GCTGTTT	370
QY	687	AAGGATGCTCTGTTACTGCGAGATGGTAATGTTGGTGGACACAGGTGAACGCAATTTG	746
Db	371	CGTGAATGCAAGCAGCTATTTGGCACTGTTTCATCCCGAGACA-RATCCGCAATTCG	429
QY	747	CATCAGCGATTCACTCCACCATGCGGGTAAAGSTGTGTCGTTGATGATTCCTG	806
Db	430	GGATATCGCATCGGAGCGCTGTGATCGCGGCTGTCCGTGGTGTATCCCGGAC	489
QY	807	GATATGCTGAAGAGACGACAGTGAAGTACTTATTTCCATPTCCATATTTCTTCTG	866
Db	490	GAGTGGCGCTCAAGGCCGCGCGGAGAGACCAACCACTGATACAGCCCC--G	546
QY	867	ACTCTGTGTTGTTCCCGGATCTTACTGAGCTGCAGCGCTGTGGAGCCGATTMACAC	926
Db	547	CAGCGGTGTGACGCCAGCGAGAGGAGCGTGAAMAAARCTGGCGCATSTGGCTGCTTAC	606
QY	927	GCTAAGTCTGTACTTTTGTTCGCGGTGCGGGCGTGAAGAAATGCTGCGCGCAGCTGT	986
Db	607	GCCACCAATATCGCCCTATGTGCGCGCAGCGCTGTG-CGCGCGCGCATTAAGARCTKCTG	665
QY	987	GAGTGGGGGAGAAATTAATCAACCGATGGGCGATGGCGTGGGTGTAACCATATCATC	1046
Db	666	GATTTTGGCGGAAGCTAAASCOCGGATTTCCACGCCCTGGCGGCGAAGAGCACGTC	725
QY	1047	CA 1048	
Db	726	GA 727	
RESULT 6			
CNS07131/C			
LOCUS	CNS07131	375 bp	DNA linear GSS 03-OCT-2001
DEFINITION	Anopheles gambiae GSS SP6 end of clone 32N20 of library NotreDame1 from strain PEST of Anopheles gambiae (African malaria mosquito), genomic survey sequence.		
ACCESSION	AL611872		
VERSION	AL611872.1	GI:15963295	
KEYWORDS			
SOURCE			
ORGANISM	Anopheles gambiae (African malaria mosquito)		
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;		
REFERENCE	Anopheles.		
AUTHORS	1 (bases 1 to 375)		
TITLE	Genoscope.		
JOURNAL	Direct Submission		
	Submitted (01-OCT-2001) Genoscope - Centre National de Sequencage : BP 191 91006 Evry cedex - FRANCE (E-mail : seque@genoscope.cns.fr		
REFERENCE	Web : www.genoscope.cns.fr		
AUTHORS	2 (bases 1 to 375)		
TITLE	Roth,C.W., Brey,P.T., Ke,Z. and Collins,F.H.		
JOURNAL	Direct Submission		
	Submitted (01-OCT-2001) BBMI, Institut Pasteur, 25, rue du Dr. Roux, Paris 75015, France		
COMMENT	This clone is from an A. gambiae BAC library provided by F.H. Collins and sequenced by Genoscope in collaboration with the		

[illegible]

FEATURES	SOURCE	Location/Qualifiers
		1..837
		/organism="Pseudomonas aeruginosa"
		/mol_type="genomic DNA"
		/strain="MSH"
		/db_xref="taxon:287"
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		/clone_lib="msh"
		/note="Environmental isolate. Whole genomic shotgun library."
BASE COUNT	169 a 293 c 240 g 135 t	
ORIGIN		
Query Match	4.6%: Score 100; DB 29; Length 837;	
Best Local Similarity	56.8%: Pred. No. 2.8e-17;	
Matches 184;	Conservative 0; Mismatches 140; Indels 0; Gaps 0;	
QY	341 CGCAGACATTAATTACACTTTGGAAAGCTCAAGTGTGAAGCAATTTATGTTTGGT	400
Db	432 CGCGAGATCTCTGTGAAACCTGGAAGCGCGGCGCTCGCCATTGCTATGGCATGT	491
QY	401 GGGTGAAGACCTTATCTGATCTGATGTCGTCCGCCAATCAGATTTAGATGGGTCA	460
Db	492 CGGGAGACACCTCAACCATGTACACGACCATCCATCCATGACAGCCGATCATAGTGGTCA	551
QY	461 CGTTGGAATGAGAGAGGGGGGGTTTGGACGCCGTGCGGAATGTTGATCAGTACAGGGGA	520
Db	552 CGTGGCCACCAAGAGGGGGCTTGGCCGGGGCCGAGTCTCAATCAGCGGACG	611
QY	521 GCTGGCAGTATGTCGTCTCTTGTGTCTGTGAACAACACACCTGATTACAGGTCTTTA	580
Db	612 CCTGACCGCTCGCCCGGCTCTGTGGACCGGACGCTGACATTCATCAACGCGCTCA	671
QY	581 TGATTGCGATGGAATGTTGGGAGAGTGTGGCATCGCTAGCCATATTCCGAGTCCCA	640
Db	672 CGAGGCCAGGCAACGCGCGCGATGTGCTTATCGCCAGCAAGAGTTTACCCCGCA	731
QY	641 GATTGTTTCAGCTTCTTCACAGA	664
Db	732 ACTGGCATGGAGTTTCCCGAGA	755
RESULT 8		
AM036130/c		
LOCUS	AM036130	538 bp mRNA linear EST 18-MAY-2001
DEFINITION	EST274506 tomato seed, TAMI Lycopersicon esculentum cDNA clone	
ACCESSION	AM036130	
VERSION	AM036130.1	GI:5894809
KEYWORDS	EST.	
SOURCE	Lycopersicon esculentum (tomato)	
ORGANISM	Lycopersicon esculentum	
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asterids; Lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.	
AUTHORS	Alcala,J., Vrebalov,J., White,R., Matera,A.L., Vision,T., Holt,I.E., Liang,F., Upton,J., Konning,C.M., Craven,M.B., Fujii,C.Y., Bowman,C.L., Neriman,W., Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley,S.D. and Giovannoni,J.	
TITLE	Generation of ESTs from tomato seed tissue	
JOURNAL	Unpublished	
COMMENT	Contact: CUGI Clemson University Genomics Institute. Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Email: http://www.genome.clemson.edu/orders/index.html 5 prime sequence. Location/Qualifiers 1..538 /organism="Lycopersicon esculentum" /mol_type="mRNA" /contig="TMA96"	
FEATURES	source	

Db 136 GCGATTGCGATGCGCAAGCGGTTCTATCTGAGCGTTTCGTTGTCGTTACAGGC 77
 QY 807 GATATGCTAAGAGAACCGAGGTGACG 835
 Db 76 GAAGTGGCGCTTAAACCTGCGCCAGAG 48

RESULT 12
 B2549561/c
 LOCUS B2549561 769 bp DNA linear GSS 17-DEC-2002
 DEFINITION pacsl-60_2172.xl pacsl-60 Pseudomonas aeruginosa genomic clone
 ACCESSION B2549561
 VERSION B2549561
 KEYWORDS GI:27153142
 SOURCE GSS.
 ORGANISM Pseudomonas aeruginosa
 Pseudomonas aeruginosa
 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

REFERENCE 1 (bases 1 to 769)
 Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.E., Hastings,M.,
 Burns,J.L., Kaul,R. and Olsen,M.V.
 Whole-Genome-Sequence variation among multiple isolates of
 Pseudomonas aeruginosa library
 J. Bacteriol., (2002) in press
 CONTACT: Chris K. Raymond
 GENOME CENTER
 UNIVERSITY OF WASHINGTON
 BOX 352145, Seattle, WA 98105-2145, USA
 TEL: 2062216954
 FAX: 2066857244
 EMAIL: cgraymond@u.washington.edu
 CLASS: shotgun.

FEATURES

Source
 1..769
 /organism="Pseudomonas aeruginosa"
 /mol_type="genomic DNA"
 /strain="1-60"
 /db_xref="taxon:287"
 /clone="pacsl-60_2172"
 /clone_lib="pacsl-60"
 /note="clinical isolate 1-60 whole genomic shotgun library."
 Class: shotgun

BASE COUNT 112 a 241 c 280 g 134 t 2 others

Query Match 4.08; Score 87.4; DB 29; Length 769;
 Best Local Similarity 49.28; Pred. No. 1,2e-13;
 Matches 285; Conservative 0; Mismatches 288; Indels 6; Gaps 2;

QY 523 TTGCAGATGCTGCTCTTGTGTCCTGGAACACACACCTGATTGAGGCTTTATG 582
 Db 599 TGAACGCTGCGCGCGGCTGTCGAGACCGGCGAGCTGACCTTCATCAACGCGGTACG 540
 QY 583 ATTGCATGCAAAATGCTGCGAAGGTGTTGGCCATGCTTACCATTTCCGAGTCCCA 642
 Db 539 AGGCCAGGCAACCGCGCCGCGATGCTGATCCGACGATCTTACCCGCAAC 480
 QY 643 TTGTGACGCTCTTCCAGAAACGATCCGAGATTTTGTTTAAGATGCTGCTGTT 702
 Db 479 TGGGCTAGGATTTCCCGAGAGAGTGCATCTCAAGCGGCTTACGCGACCTGCTGCT 420
 QY 703 ACTGCAGATGTAATGTTGTTGACAGAGGTGAAACGATTTTGCATCAGCGGATCAGT 762
 Db 419 TCTGCGAGCGAGTTCAGACGCGCGGAGCGCGGCTGCTGCGCTGCGCTGCGCC 360
 QY 763 CCAACATGCGGGGTAAAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 822
 Db 359 GCGGCTCAACCGCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 304
 QY 823 ACCGAGTGAAGTACTTATTCATTCACATTTCTTCTGAGCTGCTGCTGCTGCTGCTGCT 882
 Db 303 GCCACGGTGAAGAGACCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 244

QY 883 CGGATCTACAGAGGCTCCAGCGCTGCGAGGCGATTAAACGCGTAAGCTGTCACTT 942
 Db 243 AGCGAGCGCGAAGTCTCAGACGCTGCCCCCTGC--TGCCACGCGAAGATTCGCA 186
 QY 943 TGTCTGCGGTGCGGCGTGAAGATGCTCCGCGCGAAGTGTGAGTTGGCGGAGAGA 1002
 Db 185 TCTACGCGCGGCTGCGCGTCCAGGCGCGACGACTTCTGTGTGCTGCGCGCGCGCC 126
 QY 1003 TTAATACCGATCGCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1062
 Db 125 TCAAGCG 66
 QY 1063 TTGAGTGGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1101
 Db 65 TCAACATGGCGATGCGCGCTATGCTGCGGAGGATCTT 27

RESULT 13

B2571612
 LOCUS B2571612 830 bp DNA linear GSS 17-DEC-2002
 DEFINITION msh2_1969.xl msh Pseudomonas aeruginosa genomic clone msh2_1969,
 genomic survey sequence.

ACCESSION B2571612
 VERSION B2571612.1 GI:27206673
 KEYWORDS GSS.
 SOURCE Pseudomonas aeruginosa
 Pseudomonas aeruginosa
 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

REFERENCE 1 (bases 1 to 830)
 Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.E., Hastings,M.,
 Burns,J.L., Kaul,R. and Olsen,M.V.

Whole-Genome-Sequence variation among multiple isolates of
 Pseudomonas aeruginosa library
 J. Bacteriol., (2002) in press
 CONTACT: Chris K. Raymond
 GENOME CENTER
 UNIVERSITY OF WASHINGTON
 BOX 352145, Seattle, WA 98105-2145, USA
 TEL: 2062216954
 FAX: 2066857244
 EMAIL: cgraymond@u.washington.edu
 CLASS: shotgun.

FEATURES

Source
 1..830
 /organism="Pseudomonas aeruginosa"
 /mol_type="genomic DNA"
 /strain="msh"
 /db_xref="taxon:287"
 /clone="msh2_1969"
 /clone_lib="msh"
 /note="Environmental isolate. Whole genomic shotgun library."
 Class: shotgun

BASE COUNT 175 a 271 c 232 g 151 t 1 others

Query Match 3.98; Score 85.2; DB 29; Length 830;
 Best Local Similarity 54.38; Pred. No. 5.3e-13;
 Matches 171; Conservative 0; Mismatches 144; Indels 0; Gaps 0;

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 VERSION BH241614
 KEYWORDS Arabidopsis thaliana
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana

REFERENCE
 AUTHORS Town, C.D., Whitelaw, C.A., Pai, G., Van Aken, S.E., Utterback, J.V., Felblyum, T.V. and Fraser, C.M.
 TITLE Survey sequencing of Arabidopsis thaliana BAC F26021
 JOURNAL Unpublished
 COMMENT Contact: Chris Town
 TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdtown@tigr.org
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 VERSION BH770875.1 GI:20373832
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 SOURCE Lactococcus lactis subsp. cremoris
 ORGANISM Lactococcus lactis subsp. cremoris
 Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.

REFERENCE
 AUTHORS Bolotin, A., Ehrlich, S.D. and Sorokin, A.
 TITLE Studies of genomes of dairy bacteria Lactococcus lactis subsp. cremoris, (2002) In press
 JOURNAL Sci. Aliments, (2002) In press
 COMMENT Contact: Sorokin A
 Genetique Microbienne
 INRA
 CRJ INRA, Domaine de Vilvert, 78352 Jouy en Josas cedex, France
 Tel: 33 1 34 65 25 16
 Fax: 33 1 34 65 25 21
 Email: sorokin@jouy.inra.fr
 best homologue in strain IL1403 is poxl (99%)
 Class: shotgun
 High quality sequence start: 30
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 Db 722 TC 721

Tue Oct 7 07:11:16 2003

us-09-965-825-1.rst

Page 10

Search completed: October 3, 2003, 18:49:55
Job time : 4101 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 3, 2003, 17:41:32 : Search time 541 Seconds
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10184.593 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1708419 seqs, 1275431651 residues

Total number of hits satisfying chosen parameters: 3416838

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
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Listing first 45 summaries

Database :

Published Applications NA:*

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3	2160	100.0	2160	US-10-143-856-3	Sequence 3, Appli
4	2160	100.0	2160	US-10-078-167-6	Sequence 4, Appli
5	2160	100.0	3248	US-09-965-825-4	Sequence 1, Appli
6	2160	100.0	3309400	US-09-738-626-1	Sequence 1, Appli
7	1737	80.4	1737	US-09-738-626-2873	Sequence 2873, Ap
8	875	40.5	875	US-09-965-825-7	Sequence 3, Appli
9	875	40.5	875	US-10-1336-049-6	Sequence 6, Appli
10	875	40.5	875	US-10-143-856-5	Sequence 5, Appli
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ALIGNMENTS

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Sequence 1, Application US/09965825
Patent No. US2002015099A1
GENERAL INFORMATION:
APPLICANT: DUSCH, Nicole
APPLICANT: THOMAS, Hermann
APPLICANT: THIERBACH, Georg
TITLE OF INVENTION: PROCESS FOR THE FERMENTATIVE PREPARATION OF D-PANTOTHENIC AC
FILE REFERENCE: 2135405X
CURRENT APPLICATION NUMBER: US/09/965, 825
PRIOR FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: DE 10048604.5
PRIOR FILING DATE: 2000-09-30
PRIOR APPLICATION NUMBER: DE 10117085.8
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 2160
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
FEATURES:
NAME/KEY: CDS
LOCATION: (327)..(2063)
OTHER INFORMATION:
NAME/KEY: -35 signal
LOCATION: (227)..(223)
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LOCATION: (256)..(261)
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; APPLICANT: Hans, Stephan
; APPLICANT: Bathie, Brigitte
; APPLICANT: Beth, Alexander
; APPLICANT: Thierbach, Georg
; APPLICANT: Kreutzer, Caroline
; APPLICANT: Mockel, Bettina
; TITLE OF INVENTION: Process for the Preparation of L-Amino Acids with Amplification
; TITLE OF INVENTION: The 2nd Gene
; FILE REFERENCE: 7601/80158
; CURRENT APPLICATION NUMBER: US/10/336,049
; NUMBER OF SEQ ID NOS: 37
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; SEQ ID NO: 4
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; TYPE: DNA
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; OTHER INFORMATION: poxb
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QY 1201 TCAACGATGCGCACATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1260
Db 1201 TCAACGATGCGCACATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1260
QY 1261 CTGCAACGATGAGAAATTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1320
Db 1261 CTGCAACGATGAGAAATTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1320
QY 1321 ATCGGATGCTCAAGGCAACGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1380
Db 1321 ATCGGATGCTCAAGGCAACGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1380
QY 1381 ACGTGGAAGAGATGTGCTTATTCACCTGTGAATACGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1440
Db 1381 ACGTGGAAGAGATGTGCTTATTCACCTGTGAATACGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1440
QY 1441 CGGATTAAGAGATGTGCTTATTCACCTGTGAATACGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1500
Db 1441 CGGATTAAGAGATGTGCTTATTCACCTGTGAATACGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1500
QY 1501 ACATGGAAGATGTGCTTATTCACCTGTGAATACGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1560
Db 1501 ACATGGAAGATGTGCTTATTCACCTGTGAATACGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1560
QY 1561 CTAATGCTTGTGCTTATTCACCTGTGAATACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1620
Db 1561 CTAATGCTTGTGCTTATTCACCTGTGAATACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1620
QY 1621 CGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1680
Db 1621 CGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1680
QY 1681 ACACATTCCTGCTGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1740
Db 1681 ACACATTCCTGCTGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1740

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QY	1741	GGATGCTCGTGGAGGAGACCCAGATTTCGCTACTGACCATGAGGAAGTCAATTTCGAC	1800
Db	1741	AGATGCTCGTGGAGGAGACCCAGATTTCGCTACTGACCCATGAGGAAGTCAATTTCGAC	1800
QY	1801	AGATTGCGCGGCTGCGGGGTATCCAAATGGTACCGATACCGATCCGAAAGTTCGCG	1860
Db	1801	AGATTGCGCGGCTGCGGGGTATCCAAATGGTACCGATACCGATCCGAAAGTTCGCG	1860
QY	1861	AGCAGCTAGCTGAGGCAATTGGCATATCCCTGAGCCCTGACATGATATTCGTCACGAGTC	1920
Db	1861	AGCAGCTAGCTGAGGCAATTGGCATATCCCTGAGCCCTGACATGATATTCGTCACGAGTC	1920
QY	1921	CTAATGGCGCTTCGATCCACCAACCATCACGTGGGAACAGTGATGGATTACGAAG	1980
Db	1921	CTAATGGCGCTTCGATCCACCAACCATCACGTGGGAACAGTGATGGATTACGAAG	1980
QY	1981	CGGCGACCCCGCAACCGCTCTTGTTGGTGAGAGTAGAGGATGATGATTCGGCCCCGTTGA	2040
Db	1981	CGGCGACCCCGCAACCGCTCTTGTTGGTGAGAGTAGAGGATGATGATTCGGCCCCGTTGA	2040
QY	2041	ACATAGGAATATTCCTACTCCATGATGATTGATACACCTGCTTCCTCATTTGACCGGGA	2100
Db	2041	ACATAGGAATATTCCTACTCCATGATGATTGATACACCTGCTTCCTCATTTGACCGGGA	2100
QY	2101	GGCGTTACGTCGCAACATTTCACGAGATGGCAGCTCAGCCGCGTCCCATGAGATTGGCCT	2160
Db	2101	GGCGTTACGTCGCAACATTTCACGAGATGGCAGCTCAGCCGCGTCCCATGAGATTGGCCT	2160

RESULT 3
US-10-143-856-3

QY	1	TTAGAGGCGGATTCGTGTGAGGTCACCTTTTGTGGGCGCGGCTAAATTGGCCAGTTT	60
Db	1	TTAGAGGCGGATTCGTGTGAGGTCACCTTTTGTGGGCGCGGCTAAATTGGCCAGTTT	60
QY	61	CGAGGCGACCGACAGAGGCGTCCCGACAGCTTTTAAATGAGCCATCGGTGGCATCTGCT	120
Db	61	CGAGGCGACCGACAGAGGCGTCCCGACAGCTTTTAAATGAGCCATCGGTGGCATCTGCT	120
QY	121	TTGTGTTGACGGGCTAAACCAACACAGACTGCCGACAGCAGGAATCCCAAAAGT	180

Db	121	TTGGTTTCACGGGGCTGAAACC	AAACAGACTCCACGACAGCAAGAAATCCCAAGT	180
QY	181	GGGCATCCCGTGTGGTACCGAGT	TACCCACCCGGGCTGAAATCCTTCCCTGGCAGCGGGC	240
Db	181	GGGCATCCCGTGTGTGTACCGAGT	TACCCACCCGGGCTGAAATCCTTCCCTGGCAGCGGGC	240
QY	241	AAGCGTGGCAACACAGTGAATTTA	AGAGCAATTAAGTCGCACCCAGCTTACGAC	300
Db	241	AAGCGTGGCAACACAGTGAATTTA	AGAGCAATTAAGTCGCACCCAGCTTACGAC	300
QY	301	AATAGCCATTAAGCTTAGAGATT	TCAGATGCGACACAGTACCGAGAACATTAATGACA	360
Db	301	AATAGCCATTAAGCTTAGAGATT	TCAGATGCGACACAGTACCGAGAACATTAATGACA	360
QY	361	CTTTGGAACCTCAAGGTGGAAGC	GAATTAAGTTGGTGGGGTGCACGCTTAATCCGA	420
Db	361	CTTTGGAACCTCAAGGTGGAAGC	GAATTAAGTTGGTGGGGTGCACGCTTAATCCGA	420
QY	421	TCGTGGATGCTGTCCGCCAAT	CAGATATTGAGTGGGTGCACGTTCCGAAATGAGAGACGG	480
Db	421	TCGTGGATGCTGTCCGCCAAT	CAGATATTGAGTGGGTGCACGTTCCGAAATGAGAGACGG	480
QY	481	CGGGCTTTGACACCGGTGGGGAAT	GCTGTATCACTGCGGAGCTGGCAGTATGTCTGCTT	540
Db	481	CGGGCTTTGACACCGGTGGGGAAT	GCTGTATCACTGCGGAGCTGGCAGTATGTCTGCTT	540
QY	541	CTTGTGTCCTTGAAACACACAC	ACTGATTCAGAGGCTCTTATATATTCGCAATCGAAATGAGT	600
Db	541	CTTGTGTCCTTGAAACACACAC	ACTGATTCAGAGGCTCTTATATATTCGCAATCGAAATGAGT	600
QY	601	CGAAGGTGTGGCCATCGCTAC	CCATATTCGAGTGCACCAATTGGTTGACAGTTCCTCC	660
Db	601	CGAAGGTGTGGCCATCGCTAC	CCATATTCGAGTGCACCAATTGGTTGACAGTTCCTCC	660
QY	661	AGGAACCCATCCGAGATTTTGT	TAAAGAAATGCTCTGTTACTGCGAGTGGTAAAG	720
Db	661	AGGAACCCATCCGAGATTTTGT	TAAAGAAATGCTCTGTTACTGCGAGTGGTAAAG	720
QY	721	GTGCTGACACAGGTCACGCA	TTTGTGCATCAGCGCATTCAGTCCACCATGGCGGTAAAG	780
Db	721	GTGCTGACACAGGTCACGCA	TTTGTGCATCAGCGCATTCAGTCCACCATGGCGGTAAAG	780
QY	781	GTGCTGAGTGGTGTATGATCT	CTCGGTGATTCGCTTAAAGAAAGCAGCGTACGCTACT	840
Db	781	GTGCTGAGTGGTGTATGATCT	CTCGGTGATTCGCTTAAAGAAAGCAGCGTACGCTACT	840
QY	841	ATTCCAATTCACATATTCTT	GTGGCACTCGTGTGTCATCCCGGATCCTACTGAGCGTG	900
Db	841	ATTCCAATTCACATATTCTT	GTGGCACTCGTGTGTCATCCCGGATCCTACTGAGCGTG	900
QY	901	CAGCGCTGTGTAGAGCGCAT	TTAACAACGCTAAAGTCTGTACTTGTCTGTGCGGTGCGGGCG	960
Db	901	CAGCGCTGTGTAGAGCGCAT	TTAACAACGCTAAAGTCTGTACTTGTCTGTGCGGTGCGGGCG	960
QY	961	TGAAGAATGCTCGGCGCAG	GTGTGGAGTTGGGGGAAGAATTAAATACCGAGTCGGGC	1020
Db	961	TGAAGAATGCTCGGCGCAG	GTGTGGAGTTGGGGGAAGAATTAAATACCGAGTCGGGC	1020
QY	1021	ATGCGCTGGGTGTAGACAGT	TACATCCAGCATGGAATCCCTTTGAGGTGCGGCATGTG	1080
Db	1021	ATGCGCTGGGTGTAGACAGT	TACATCCAGCATGGAATCCCTTTGAGGTGCGGCATGTG	1080
QY	1081	GCCGTGTGTGTAGAGCGCC	TGCGGTGATGTGCTCAATGAGCGGATGTGCTGATTTCTAT	1140
Db	1081	GCCGTGTGTGTAGAGCGCC	TGCGGTGATGTGCTCAATGAGCGGATGTGCTGATTTCTAT	1140
QY	1141	TGGGTAGAGATTCCTTATTC	TATTCCTTCCCTTAAGAACAAGTTTCCACAGGTGGATTA	1200
Db	1141	TGGGTAGAGATTCCTTATTC	TATTCCTTCCCTTAAGAACAAGTTTCCACAGGTGGATTA	1200
QY	1201	TCAACGTGCGCAATTGTG	TACAGTACCAACGCTGGAAGTATCCGGTGACCGGTATGTG	1260
Db	1201	TCAACGTGCGCAATTGTG	TACAGTACCAACGCTGGAAGTATCCGGTGACCGGTATGTG	1260

Db 1201 TCAAGGTTGCGACATTTGTCAGCTACACGCTGAATATCCGCTGACCGGTGATGTTG 1260
 QY 1261 CTGCAACAATGCAAAATATTTGCTCATATGAGAGAAAAACAGATGTTCTCTCTTG 1320
 Db 1261 CTGCAACAATGCAAAATATTTGCTCATATGAGAGAAAAACAGATGTTCTCTCTTG 1320
 QY 1321 ATCGGATGCTCAAGGACACAGAGCTAAGTTGAGTGGTGTAGAGAGTACACACTA 1380
 Db 1321 ATCGGATGCTCAAGGACACAGAGCTAAGTTGAGTGGTGTAGAGAGTACACACTA 1380
 QY 1381 ACCTGAGAGATGCTGCTATTCACCTGAATACCTGCTCTATTTTGAACGAGCTG 1440
 Db 1381 ACCTGAGAGATGCTGCTATTCACCTGAATACCTGCTCTATTTTGAACGAGCTG 1440
 QY 1441 CGGATAGAGATGCTGCTATTCACCTGAATACCTGCTCTATTTTGAACGAGCTG 1500
 Db 1441 CGGATAGAGATGCTGCTATTCACCTGAATACCTGCTCTATTTTGAACGAGCTG 1500
 QY 1501 ACATGAGAGATGCTGCTATTCACCTGAATACCTGCTCTATTTTGAACGAGCTG 1560
 Db 1501 ACATGAGAGATGCTGCTATTCACCTGAATACCTGCTCTATTTTGAACGAGCTG 1560
 QY 1561 CTAAATGCTGCTCATGATGATGTTGGGCAAAAGTTGATGCAAAACCGCAGGTATG 1620
 Db 1561 CTAAATGCTGCTCATGATGATGTTGGGCAAAAGTTGATGCAAAACCGCAGGTATG 1620
 QY 1621 CGATGCTGCTCATGATGATGTTGGGCAAAAGTTGATGCAAAACCGCAGGTATG 1680
 Db 1621 CGATGCTGCTCATGATGATGTTGGGCAAAAGTTGATGCAAAACCGCAGGTATG 1680
 QY 1681 ACCAATGCTGCTCATGATGATGTTGGGCAAAAGTTGATGCAAAACCGCAGGTATG 1740
 Db 1681 ACCAATGCTGCTCATGATGATGTTGGGCAAAAGTTGATGCAAAACCGCAGGTATG 1740
 QY 1741 AGATGCTGCTCATGATGATGTTGGGCAAAAGTTGATGCAAAACCGCAGGTATG 1800
 Db 1741 AGATGCTGCTCATGATGATGTTGGGCAAAAGTTGATGCAAAACCGCAGGTATG 1800
 QY 1801 AGATGCTGCTCATGATGATGTTGGGCAAAAGTTGATGCAAAACCGCAGGTATG 1860
 Db 1801 AGATGCTGCTCATGATGATGTTGGGCAAAAGTTGATGCAAAACCGCAGGTATG 1860
 QY 1861 AGAGCTGCTCATGATGATGTTGGGCAAAAGTTGATGCAAAACCGCAGGTATG 1920
 Db 1861 AGAGCTGCTCATGATGATGTTGGGCAAAAGTTGATGCAAAACCGCAGGTATG 1920
 QY 1921 CTAAATGCTGCTCATGATGATGTTGGGCAAAAGTTGATGCAAAACCGCAGGTATG 1980
 Db 1921 CTAAATGCTGCTCATGATGATGTTGGGCAAAAGTTGATGCAAAACCGCAGGTATG 1980
 QY 1981 CGGCTGCTCATGATGATGTTGGGCAAAAGTTGATGCAAAACCGCAGGTATG 2040
 Db 1981 CGGCTGCTCATGATGATGTTGGGCAAAAGTTGATGCAAAACCGCAGGTATG 2040
 QY 2041 ACATAAGATATTTCTCTCATGATGATGTTGGGCAAAAGTTGATGCAAAACCGCAGGTATG 2100
 Db 2041 ACATAAGATATTTCTCTCATGATGATGTTGGGCAAAAGTTGATGCAAAACCGCAGGTATG 2100
 QY 2101 GCGCTTAACTGCAAAATTTTGAAGATGATGTTGGGCAAAAGTTGATGCAAAACCGCAGGTATG 2160
 Db 2101 GCGCTTAACTGCAAAATTTTGAAGATGATGTTGGGCAAAAGTTGATGCAAAACCGCAGGTATG 2160

RESULT 4
 US-10-078-167-4
 ; Sequence 4, Application US/10078167
 ; Publication No. US20030119154A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Danican, Rita
 ; APPLICANT: McCormack, Ashling
 ; APPLICANT: Stapleton, Cliona
 ; APPLICANT: Burke, Kevin
 ; APPLICANT: Mockel, Bettina

TITLE OF INVENTION: Process for the preparation of L-amino acids using
 FILE REFERENCE: 990229 BT-US-B
 CURRENT APPLICATION NUMBER: US/10/078.167
 CURRENT FILING DATE: 2002-02-20
 NUMBER OF SEQ ID NOS: 16
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 4
 LENGTH: 2160
 TYPE: DNA
 ORGANISM: Corynebacterium glutamicum
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (327)..(2063)
 OTHER INFORMATION: poxb
 US-10-078-167-4

Query Match 100.0%; Score 2160; DB 14; Length 2160;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TTAAAGCGATTTCTGAGTCACTTTTGGGGTGGGGTCTAAATTTGGCGATTT 60
 1 TTAAAGCGATTTCTGAGTCACTTTTGGGGTGGGGTCTAAATTTGGCGATTT 60
 61 CGAGGCGACGACAGGCGTCCCGACGATGTTTAAATAGGAGATCGGTGGCATCTGT 120
 61 CGAGGCGACGACAGGCGTCCCGACGATGTTTAAATAGGAGATCGGTGGCATCTGT 120
 121 TTGGTTTGACAGGCGTGAACCAACAGACTGCCGACGACCAAGCGGAATCCAAAGT 180
 121 TTGGTTTGACAGGCGTGAACCAACAGACTGCCGACGACCAAGCGGAATCCAAAGT 180
 181 GGGCATCCCTGTTTGTATACGATACCCACCGCGCTGAACCTCCCTGACGCGGGCG 240
 181 GGGCATCCCTGTTTGTATACGATACCCACCGCGCTGAACCTCCCTGACGCGGGCG 240
 241 AAGCGTGGCAACAACCTGGAATTTAAGAGCACATTTAAGTGCACCAAGTTAGCAAC 300
 241 AAGCGTGGCAACAACCTGGAATTTAAGAGCACATTTAAGTGCACCAAGTTAGCAAC 300
 301 AATAGCCATACGTTGAGAGATGAGATGAGACAGTACAGCAACCAATTAATGACA 360
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 361 CTTTGGAGCTCAAGAGTGTGAAGCAATTTATGTTGGTGGTGTGACAGCTTAATCGA 420
 361 CTTTGGAGCTCAAGAGTGTGAAGCAATTTATGTTGGTGGTGTGACAGCTTAATCGA 420
 421 TCGTGATGCTGTCGCGCAATCAGATATGAGTGGTGGTGGTGGTGGTGGTGGTGGT 480
 421 TCGTGATGCTGTCGCGCAATCAGATATGAGTGGTGGTGGTGGTGGTGGTGGTGGT 480
 481 CGGCTTGAAGCGGTGCGCAATGTTGATCACTGGGAGCTGGCAGTATGTCCTCT 540
 481 CGGCTTGAAGCGGTGCGCAATGTTGATCACTGGGAGCTGGCAGTATGTCCTCT 540
 541 CTTGTTGCTCTGGAACACACACTGATGAGGCTCTTATGATGCTGATGCAATGATG 600
 541 CTTGTTGCTCTGGAACACACACTGATGAGGCTCTTATGATGCTGATGCAATGATG 600
 601 CGAAGGTTGGGCGATGCTAGCCATATTCGAGATGCGCCAGATTTGTTGAGTTCCT 660
 601 CGAAGGTTGGGCGATGCTAGCCATATTCGAGATGCGCCAGATTTGTTGAGTTCCT 660
 661 AGGAAGCGATTCGAGATTTTGTATGAAGATCTCTGTTACTGCGAGATGATG 720
 661 AGGAAGCGATTCGAGATTTTGTATGAAGATCTCTGTTACTGCGAGATGATG 720
 721 GTGGTGAAGAGGATGAGATTTTGAATGATGAGATGATGATGATGATGATGATGATG 780
 721 GTGGTGAAGAGGATGAGATTTTGAATGATGAGATGATGATGATGATGATGATGATG 780

OY	781	TGTGTCGGCTGATGAATTCCCGTATACGCTAAGAGAAGCAGCGTAGCTACT	840
Db	781	GTTGTGCGTGTAAGTAATTCCTGTGTATACGCTAAAGAAAGCAGGTACGGTACTT	840
OY	841	ATTCCAAATTCACATAATTTCTTCTGTGCACACTCTGTGATGTTCGCCGATCCCTACTAGGCTG	900
Db	841	ATTCCAAATTCACATAATTTCTTCTGTGCACACTCTGTGATGTTCGCCGATCCCTACTAGGCTG	900
OY	901	CAGCGCTGTGTGAGGCGAATTACAACCGCTAAGTGTGTCACTTTTCTGTGCGGTGCGGCG	960
Db	901	CAGCGCTGTGTGAGGCGCATTTAACAAACCTAAGTGTGTCACTTTTCTGTGCGGTGCGGCG	960
OY	961	TGAAGAAATGCTCGGGCGAGGTGTGTGAGTTGGGGGGAATATAATACCAGTCCGGC	1020
Db	961	TGAAGAAATGCTCGGGCGAGGTGTGTGAGTTGGGGGGAATATAATACCAGTCCGGC	1020
OY	1021	ATGGCGCTGGGTGTAGACAGTACATCCAGCATGGAATCCGTTTGAGTCCGCGCATGTCTG	1080
Db	1021	ATGGCGCTGGGTGTAGACAGTACATCCAGCATGGAATCCGTTTGAGTCCGCGCATGTCTG	1080
OY	1081	GCCTGCTTGGTTAGCGGCGCTGCTGTGATGTGTCATGAGCGCGATCTGTGATTTCTAT	1140
Db	1081	GCCTGCTTGGTTAGCGGCGCTGCTGTGATGTGTCATGAGCGCGATCTGTGATTTCTAT	1140
OY	1141	TGGGTACGGAATTTCCCTTATTCATATTTCCTTCCCTAAAGACAGGTTGCCAGATGATA	1200
Db	1141	TGGGTACGGAATTTCCCTTATTCATATTTCCTTCCCTAAAGACAGGTTGCCAGATGATA	1200
OY	1201	TCAAAGGTGGCACATTTGTGTGACGTACACAGGTGAAGTATCCGGTACCGGCTATGTTG	1260
Db	1201	TCAAAGGTGGCCACATTTGTGTGACGTACACAGGTGAAGTATCCGGTACCGGCTATGTTG	1260
OY	1261	CTGCACACATTCGAAAAATTTTGGCTCATGTGAAGAAAAAACAAGATCGTTCCTCTTG	1320
Db	1261	CTGCACACATTCGAAAAATTTTGGCTCATGTGAAGAAAAAACAAGATCGTTCCTCTTG	1320
OY	1321	ATCGGATGCTTAAGGCAACAGSAGTAAAGTTAGCTCGGTGTAGAGACGTACACACATA	1380
Db	1321	ATCGGATGCTTAAGGCAACAGSAGTAAAGTTAGCTCGGTGTAGAGACGTACACACATA	1380
OY	1381	ACGTGAGAAACATGTGCTTATTCACCTGTAATCCGTTGCGCTCATTTTGAACAGCTGG	1440
Db	1381	ACGTGAGAAACATGTGCTTATTCACCTGTAATCCGTTGCGCTCATTTTGAACAGCTGG	1440
OY	1441	CGGATTAAGGATGCGGTGTTTACTGTGTGATACCGGCATGTGCATATGTGGATGCGAGGT	1500
Db	1441	CGGATTAAGGATGCGGTGTTTACTGTGTGATACCGGCATGTGCATATGTGGATGCGAGGT	1500
OY	1501	ACATCGAAGATCCGSGAGGAACGGCGCATTTGTGGTTCATTTCCGCCACGGCACGATGG	1560
Db	1501	ACATCGAAGATCCGSGAGGAACGGCGCATTTGTGGTTCATTTCCGCCACGGCACGATGG	1560
OY	1561	CTAATGCGTTCCCTCATCGCATTTGTTGGTGGCAAACTGTGTGATCGAAACCGCAGGTGATCG	1620
Db	1561	CTAATGCGTTCCCTCATCGCATTTGTTGGTGGCAAACTGTGTGATCGAAACCGCAGGTGATCG	1620
OY	1621	CGATGTGTGGGATGATGTGTTGGGCACTGCTGCTGGGTGAGCTTCTGACCGTTTAAGCTGC	1680
Db	1621	CGATGTGTGGGATGATGTGTTGGGCACTGCTGCTGGGTGAGCTTCTGACCGTTTAAGCTGC	1680
OY	1681	ACCACACTTCCCTTAAGAGCTGTGTTTAAACAAGATCTTTTGGGATGGTGAAGTTGG	1740
Db	1681	ACCACACTTCCCTTAAGAGCTGTGTTTAAACAAGATCTTTTGGGATGGTGAAGTTGG	1740
OY	1741	AGATGCTGTGTGAGGGAACGCAGAAATTTGTTACTGACCATGAGAAAGTAAATTCGAG	1800
Db	1741	AGATGCTGTGTGAGGGAACGCAGAAATTTGTTACTGACCATGAGAAAGTAAATTCGAG	1800
OY	1801	AGATTGGCGCGCTCGCGGTATTCAAATTCGGTACCATACCGATCCGAAAGAAATTTGCGG	1860
Db	1801	AGATTGGCGCGCTCGCGGTATTCAAATTCGGTACCATACCGATCCGAAAGAAATTTGCGG	1860
OY	1861	AGCAGTACCTGAGCAATTGGCANATCTCTGAGCTGTACTGATGATATCGTCCAGATC	1920

Db	1861	AGCAGCTAGGAGCATTTGGATATTCTTGACCTGTACTGATGATATCGTCAGGATTC	1920
Qy	1921	CTAATGCGCTGTGCATATCCACCACAACCATCACGTGGGAACAGTGCATGGATTCAGCAAG	1980
Db	1921	CTAATGCGCTGTGCATATCCACCACAACCATCACGTGGGAACAGTGCATGGATTCAGCAAG	1980
Qy	1981	CGGCCACCCGAAACCGCTCTTTGGTGAGAGTAGAGAGCGATGATGATCTGSCCCGTTGCA	2040
Db	1981	CGGCCACCCGAAACCGCTCTTTGGTGAGAGTAGAGAGCGATGATGATCTGSCCCGTTGCA	2040
Qy	2041	ACATAGGAATAATTTCTCTACTCATGATGATGATGATACACTGCTGTTCATTTGACCGGGA	2100
Db	2041	ACATAGGAATAATTTCTCTACTCATGATGATGATGATACACTGCTGTTCATTTGACCGGGA	2100
Qy	2101	GCGCTTAAC TGCCCAACATTTCCAGAGTGGCAGCTACGCCGCTGGCCCATGAGATTGCCCT	2160
Db	2101	GCGCTTAAC TGCCCAACATTTCCAGAGTGGCAGCTACGCCGCTGGCCCATGAGATTGCCCT	2160
<hr/>			
RESULT 5			
US-09-965-825-4			
Sequence 4, Application US/09965825			
Patent No. US2002015099A1			
GENERAL INFORMATION:			
APPLICANT: DUSCH, Nicole			
APPLICANT: THOMAS, Hermann			
APPLICANT: THERBACH, Georg			
TITLE OF INVENTION: PROCESS FOR THE FERMENTATIVE PREPARATION OF D-PANTOTHENIC ACID			
FILE REFERENCE: 21354DSOX			
CURRENT APPLICATION NUMBER: US/09/965_825			
CURRENT FILING DATE: 2001-10-01			
PRIOR APPLICATION NUMBER: DE 10048604_5			
PRIOR FILING DATE: 2000-09-30			
PRIOR APPLICATION NUMBER: DE 10117085_8			
PRIOR FILING DATE: 2001-04-06			
NUMBER OF SEQ ID NOS: 14			
SOFTWARE: PatentIn version 3.1			
SEQ ID NO 4			
LENGTH: 3248			
TYPE: DNA			
ORGANISM: Corynebacterium glutamicum			
FEATURE:			
NAME/KEY: CDS			
LOCATION: (802)..(2538)			
OTHER INFORMATION:			
US-09-965-825-4			
<hr/>			
Query Match			
Best Local Similarity 100.0%; Score 2160; DB 10; Length 3248;			
Matches 2160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	TTAGAGCGGATTTCTGTGAGTCACTTTTGTGGGGTGGGGTCTAAATTTGGCCAGTTTT	60
Db	476	TTAGAGCGGATTTCTGTGAGTCACTTTTGTGGGGTGGGGTCTAAATTTGGCCAGTTTT	535
Qy	61	CGAGSGACACAGACAGCGGCTGCCACGATTTTAAATPAGGGGATGGTGGGATCTGTGT	120
Db	536	CGAGSGACACAGACAGCGGCTGCCACGATTTTAAATPAGGGGATGGTGGGATCTGTGT	595
Qy	121	TTGGTTTGACGGGCTGAACCAAACAGACTGCCAGACCAACGACGAAATCCAAAAGT	180
Db	596	TTGGTTTGACGGGCTGAACCAAACAGACTGCCAGACCAACGACGAAATCCAAAAGT	655
Qy	181	GGGCGATCCCTGTTTGTACCGAGTACCCAGCCGGGCTGAAATCCCGGAGGCGGCG	240
Db	656	GGGCGATCCCTGTTTGTACCGAGTACCCAGCCGGGCTGAAATCCCGGAGGCGGCG	715
Qy	241	AAGCGTGGCAACAACCTGGAATTTAAGAGCACAAATTTGAAGTGGCAACAGTTAGGCAAC	300
Db	716	AAGCGTGGCAACAACCTGGAATTTAAGAGCACAAATTTGAAGTGGCAACAGTTAGGCAAC	775

QY	301	AATAGCCATAAGCTTGAGAGTTCCAGATGGCACACAGCTACGCGAACAATTAATTGACA	360
Db	776	AATAGCCATAAGCTTGAGAGTTCCAGATGGCACACAGCTACGCGAACAATTAATTGACA	835
QY	361	CTTTGGAACCTCAAGGTGTGAAGCCGAAATTATGGTTGGTGGGTACAGCCTTAATCCGA	420
Db	836	CTTTGGAACCTCAAGGTGTGAAGCCGAAATTATGGTTGGTGGGTACAGCCTTAATCCGA	895
QY	421	TGCTGGAATCTGTCCGCCAATCAGATATTGAGTGGGTGCACCTTGGAAATGAGAAACGG	480
Db	896	TGCTGGAATCTGTCCGCCAATCAGATATTGAGTGGGTGCACCTTGGAAATGAGAAACGG	955
QY	481	CGGCGTTTCACCCGGGTGCGGAAATCGTTGATCATTGGGAGCTGGCAGATATGTGCTCTT	540
Db	956	CGGCGTTTCACCCGGGTGCGGAAATCGTTGATCATTGGGAGCTGGCAGATATGTGCTCTT	1015
QY	541	CTTGTTGGTCTCTGAAACAACACCCGATTCAGGGGCTTTATGATTCGATGGAATGGTG	600
Db	1016	CTTGTTGGTCTCTGAAACAACACCCGATTCAGGGGCTTTATGATTCGATGGAATGGTG	1075
QY	601	CGAAGGTGTTGGCCATCCGCTAGCCATATTCGAGAGCCCAATTTGGTTCGAGCTTTCC	660
Db	1076	CGAAGGTGTTGGCCATCCGCTAGCCATATTCGAGAGCCCAATTTGGTTCGAGCTTTCC	1135
QY	661	AGGAACCCGATCCGGAAGATTTTGTTTAAGAATGCTCTGTTTACTGCGAGATGATG	720
Db	1136	AGGAACCCGATCCGGAAGATTTTGTTTAAGAATGCTCTGTTTACTGCGAGATGATG	1195
QY	721	GTGGTACACAGGATGAACGCAATTTTGGCATACGCGAATTCACCTCCACATGGCGGTAAG	780
Db	1196	GTGGTACACAGGATGAACGCAATTTTGGCATACGCGAATTCACCTCCACATGGCGGTAAG	1255
QY	781	GTGTGTGCGGTGATGATGATTCCTGTGTATATCGCTTAAGAGACGACAGTACGGTACTT	840
Db	1256	GTGTGTGCGGTGATGATGATTCCTGTGTATATCGCTTAAGAGACGACAGTACGGTACTT	1315
QY	841	ATTCGAATTCACATATTTCTTCTGGCACTCCTGTGGTGTCCCGAATCCTACTGAGGCTG	900
Db	1316	ATTCGAATTCACATATTTCTTCTGGCACTCCTGTGGTGTCCCGAATCCTACTGAGGCTG	1375
QY	901	CAGCGCTGTGAGAGCGATTTAACAAAGCTAAGTGTGCATCTTCTCGGGTGGGCGGCG	960
Db	1376	CAGCGCTGTGAGAGCGATTTAACAAAGCTAAGTGTGCATCTTCTCGGGTGGGCGGCG	1435
QY	961	TGAAGATGCTCGCGCGCAGGTGTTGAGTTGGCGGAGAAATTAATCAACCGATCGGGC	1020
Db	1436	TGAAGATGCTCGCGCGCAGGTGTTGAGTTGGCGGAGAAATTAATCAACCGATCGGGC	1495
QY	1021	ATGGCGTGGGTGTGAACAGTACATCCAGCATAGAAATCCGTTTGAAGTGGCATGTCTG	1080
Db	1496	ATGGCGTGGGTGTGAACAGTACATCCAGCATAGAAATCCGTTTGAAGTGGCATGTCTG	1555
QY	1081	GCGTGTGTGTGACGGGCGCTGCGTGGATGGTGCATATGAGCGGGATCTGCTGATTCAT	1140
Db	1556	GCGTGTGTGTGACGGGCGCTGCGTGGATGGTGCATATGAGCGGGATCTGCTGATTCAT	1615
QY	1141	TGGGTACGGAATTCCTTATTCGTATTCCTTCCCTTAAGACAACGTTGGCCAGGTGATA	1200
Db	1616	TGGGTACGGAATTCCTTATTCGTATTCCTTCCCTTAAGACAACGTTGGCCAGGTGATA	1675
QY	1201	TCAACGGTGGCGACATTTGGTGCAGATACCAACGGTGAAGTATCCGGTACCGGTGATGTG	1260
Db	1676	TCAACGGTGGCGACATTTGGTGCAGATACCAACGGTGAAGTATCCGGTACCGGTGATGTG	1735
QY	1261	CTGCAACAATCGAAAAATATTTGGCTCATATGGAAGAAAAACAGATCGTTCTTCTTG	1320
Db	1736	CTGCAACAATCGAAAAATATTTGGCTCATATGGAAGAAAAACAGATCGTTCTTCTTG	1795
QY	1321	ATCGGATGCTCAAAGCACACAGACGTAAGTTGAGCTCGGCTAGAGACGTATACACATA	1380
Db	1796	ATCGGATGCTCAAAGCACACAGACGTAAGTTGAGCTCGGCTAGAGACGTATACACATA	1855
QY	1381	ACGTGGAAGAGCATGTGTCCATTACACCCGTAATACCTTGGCTTATTTTGAACGAGCTGG	1440

Db	1856	ACGTGAGAGAAAGCATGTGGCTATTACACCTGAAATACGTTGCTCTATTTTGGACGAGCTGG	1915
QY	1441	CGGATPAAGGATCCGGTGTCTTACTGTGATACCGGCATGTGCAATGTGGCATCGAGGT	1500
Db	1916	CGGATPAAGGATCCGGTGTCTTACTGTGATACCGGCATGTGCAATGTGGCATCGAGGT	1975
QY	1501	ACATGAGAAATCCGAGGGAACCGCCGCACTTGTGGTTCAATCCGCCACGGCACGATGG	1560
Db	1976	ACATGAGAAATCCGAGGGAACCGCCGCACTTGTGGTTCAATCCGCCACGGCACGATGG	2035
QY	1561	CTAATGCCGTTGGCTCATATCGATTGTGGCGCAAAAGTGTGATCGAAACCGCAGGATGCG	1620
Db	2036	CTAATGCCGTTGGCTCATATCGATTGTGGCGCAAAAGTGTGATCGAAACCGCAGGATGCG	2095
QY	1621	CGATGTGTGGCATGTGTGGTTGGGCATGTGCTGGTGTGAAGCTTCTGACCGTTAAGCTGC	1680
Db	2096	CGATGTGTGGCATGTGTGGTTGGGCATGTGCTGGTGTGAAGCTTCTGACCGTTAAGCTGC	2155
QY	1681	ACCAACTTCCGGTGAAGGCTGTGGGTTTAAACAACAGTCTTTGGGCATGCTGAAAGTTGG	1740
Db	2156	ACCAACTTCCGGTGAAGGCTGTGGGTTTAAACAACAGTCTTTGGGCATGCTGAAAGTTGG	2215
QY	1741	AGATGCTGTGAGGAGACAGCCAGATTGTGTACTGACATGAGAGAAGTGAATTTCGACG	1800
Db	2216	AGATGCTGTGAGGAGACAGCCAGATTGTGTACTGACATGAGAGAAGTGAATTTCGACG	2275
QY	1801	AGATTGCCGGCGGCTGTGGGCTATCCAAATCGTACCCATACCAGATCCGAAAGAAAGTTGCGG	1860
Db	2276	AGATTGCCGGCGGCTGTGGGCTATCCAAATCGTACCCATACCAGATCCGAAAGAAAGTTGCGG	2335
QY	1861	AGCAGCTGTGAGGACATTTGGCATATCCTGGACCTGTACATGATGATATGTACAGGATC	1920
Db	2336	AGCAGCTGTGAGGACATTTGGCATATCCTGGACCTGTACATGATGATATGTACAGGATC	2395
QY	1921	CTAATGCCGCTTGTGATCCCAACAACATCAAGTGGGAACAGTGCATGGATTTGACGAAGG	1980
Db	2396	CTAATGCCGCTTGTGATCCCAACAACATCAAGTGGGAACAGTGCATGGATTTGACGAAGG	2455
QY	1981	CGGCGACCCGGAACCGTCTTGTGGTGAAGAGTAGGAGGAGATGATCTGTGGCCGTTTCCA	2040
Db	2456	CGGCGACCCGGAACCGTCTTGTGGTGAAGAGTAGGAGGAGATGATCTGTGGCCGTTTCCA	2515
QY	2041	ACATPAAGAAATTTCTACTCTCATGATGTGATATACACCTGCTGTTCTCAATPAACCGCGA	2100
Db	2516	ACATPAAGAAATTTCTACTCTCATGATGTGATATACACCTGCTGTTCTCAATPAACCGCGA	2575
QY	2101	GCGCTTAAGTCCCAACATTTTCCAGAGATGGCAGCTCACGCGGTGCCATGATGTGCCCT	2160
Db	2576	GCGCTTAAGTCCCAACATTTTCCAGAGATGGCAGCTCACGCGGTGCCATGATGTGCCCT	2635
RESULT 6			
US-09-738-626-1/c			
; Sequence 1, Application US/09738626			
; Publication No. US20020197605A1			
; GENERAL INFORMATION:			
; APPLICANT: NAKAGAMA, SATOSHI			
; APPLICANT: MIKOGUCHI, HIROSHI			
; APPLICANT: ANDO, SEIKO			
; APPLICANT: HAYASHI, MIKIRO			
; APPLICANT: OCHIAI, KEIKO			
; APPLICANT: YOKOI, HARUHIKO			
; APPLICANT: TATEISHI, NAOKO			
; APPLICANT: SENOH, AKIHIRO			
; APPLICANT: IKEDA, MASATO			
; APPLICANT: OZAKI, AKIO			
; TITLE OP INVENTION: NOVEL POLYNUCLEOTIDES			
; FILE REFERENCE: 249-125			
; CURRENT APPLICATION NUMBER: US/09/738, 626			
; CURRENT FILING DATE: 2000-12-18			
; PRIOR APPLICATION NUMBER: JP 99/377484			
; PRIOR FILING DATE: 1999-12-16			

PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 1
LENGTH: 3309400
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
US-09-738-626-1

Query Match 100.0%; Score 2160; DB 10; Length 3309400;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 TTAGAGGCGATTCGTGAGGTCACCTTTTGTGGGCGGGGCTAAATTGGCCAGTTT 60
Db 2778830 TTAGAGGCGATTCGTGAGGTCACCTTTTGTGGGCGGGGCTAAATTGGCCAGTTT 2778771

QY 61 CGAGGCGACACGACAGGCGTCCACGATGTTTAAATAGGCGATCGGTGGGATCTGTGT 120
Db 2778770 CGAGGCGACACGACAGGCGTCCACGATGTTTAAATAGGCGATCGGTGGGATCTGTGT 2778711

QY 121 TTGGTTTCGAGGGGCTGAACCAACACAGACCTGCCAGACAGAGGAAATCCCAAAAT 180
Db 2778710 TTGGTTTCGAGGGGCTGAACCAACACAGACCTGCCAGACAGAGGAAATCCCAAAAT 2778651

QY 181 GGGCATCCCTGTTTGTGTAACGAGTACCCACCCGGGCTGAACCTCCCTGGCAGCGGGG 240
Db 2778650 GGGCATCCCTGTTTGTGTAACGAGTACCCACCCGGGCTGAACCTCCCTGGCAGCGGGG 2778591

QY 241 AAGCGTGGCAACACTGGAATTTAAGGACATTAAGTCGACACAGTAACTAGGCAACAC 300
Db 2778590 AAGCGTGGCAACACTGGAATTTAAGGACATTAAGTCGACACAGTAACTAGGCAACAC 2778531

QY 301 AATAGCCATACGTTGAGAGGTTAGATGCGACACAGCTACGACAGCAATTAATGACA 360
Db 2778530 AATAGCCATACGTTGAGAGGTTAGATGCGACACAGCTACGACAGCAATTAATGACA 2778471

QY 361 CTTTGGAGCTCAAGGTGTGAAGCAATTTATGTTTGGGTGACAGCTTAATCCGA 420
Db 2778470 CTTTGGAGCTCAAGGTGTGAAGCAATTTATGTTTGGGTGACAGCTTAATCCGA 2778411

QY 421 TCGTGAATGCTCCGCAATCAGATATTGAGTGGTGCACGTTCAAAATGAGAGACGG 480
Db 2778410 TCGTGAATGCTCCGCAATCAGATATTGAGTGGTGCACGTTCAAAATGAGAGACGG 2778351

QY 481 CGGCGTTTGCAGCCGGTGGGATCGTTGATCTGCTGGAGCTGGCAGTATGTCTCT 540
Db 2778350 CGGCGTTTGCAGCCGGTGGGATCGTTGATCTGCTGGAGCTGGCAGTATGTCTCT 2778291

QY 541 CTTGTGCTCTGGAACACACACCTGATTAGGGTCTTTATGATTGCAATCGAAATGTTG 600
Db 2778290 CTTGTGCTCTGGAACACACACCTGATTAGGGTCTTTATGATTGCAATCGAAATGTTG 2778231

QY 601 CGAAGGTGTTGGCCATGCTAGCCATATTCGAGTCCGACAGATGTTGTTGACGTTCTCC 660
Db 2778230 CGAAGGTGTTGGCCATGCTAGCCATATTCGAGTCCGACAGATGTTGTTGACGTTCTCC 2778171

QY 661 AGGAAACGATCCGAGATTTTGTAAAGATGCTGTTTCTGCTGAGATGCTGAAG 720
Db 2778170 AGGAAACGATCCGAGATTTTGTAAAGATGCTGTTTCTGCTGAGATGCTGAAG 2778111

QY 721 GTGGTGAAGAGGTTGAACGATTTTGCATACGCGATTGCTGACCATGCGGGTAAAG 780
Db 2778110 GTGGTGAAGAGGTTGAACGATTTTGCATACGCGATTGCTGACCATGCGGGTAAAG 2778051

QY 781 GTGTGCGGTGTAGTATCTGTGATATCTGCTAAGAAAGACGAGGTGAGGTACTT 840
Db 2778050 GTGTGCGGTGTAGTATCTGTGATATCTGCTAAGAAAGACGAGGTGAGGTACTT 2777991

QY 841 ATTCAATTCACATATTTCTTTCGCACTCCTGTGTTCCCGAGTCTACTGAGGCTG 900
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Db 2777990 ATTCAATTCACATATTTCTTCTGCACTCCTGTGTTCCCGATCTACTGAGGCTG 2777931
QY 901 CAGCGCTGTGAGGCGAATTAAACAGCTAGTCTGCTACTTTGTTCTGGGTGGGCG 960
Db 2777930 CAGCGCTGTGAGGCGAATTAAACAGCTAGTCTGCTACTTTGTTCTGGGTGGGCG 2777871

QY 961 TGAAGATGCTGCGCGAGGCTGTGATGAGTGGCGGAGAAATTAATCAGCATCGGCG 1020
Db 2777870 TGAAGATGCTGCGCGAGGCTGTGATGAGTGGCGGAGAAATTAATCAGCATCGGCG 2777811

QY 1021 ATGCGCTGGGTGTGAAGCATATCAGCATGAGATTCGTTGAGGTGGCATGTCTG 1080
Db 2777810 ATGCGCTGGGTGTGAAGCATATCAGCATGAGATTCGTTGAGGTGGCATGTCTG 2777751

QY 1081 GCCTGCTGTGTACGCGCGCTGCGGATGCTGCAATGAGGCGGATGCTGATTTAT 1140
Db 2777750 GCCTGCTGTGTACGCGCGCTGCGGATGCTGCAATGAGGCGGATGCTGATTTAT 2777691

QY 1141 TTGGTACGGAATTCCTTATTCGTGATTTCTCTTCTTAAGACACCTTCCGAGTGATA 1200
Db 2777690 TTGGTACGGAATTCCTTATTCGTGATTTCTCTTCTTAAGACACCTTCCGAGTGATA 2777631

QY 1201 TCAAGCGTGGCAGATTTGGTGGAGCTGACACGCTGAAGTATCCGGTGAATGTG 1260
Db 2777630 TCAAGCGTGGCAGATTTGGTGGAGCTGACACGCTGAAGTATCCGGTGAATGTG 2777571

QY 1261 CTGCAACAATCGAAATATTTTCTCTCATGTGAAGAAACACATGCTCTCTCTG 1320
Db 2777570 CTGCAACAATCGAAATATTTTCTCTCATGTGAAGAAACACATGCTCTCTCTG 2777511

QY 1321 ATCGATGCTCAAGGACACAGCGCTAAGTTAGCTGGTGTGAAGACATACACATA 1380
Db 2777510 ATCGATGCTCAAGGACACAGCGCTAAGTTAGCTGGTGTGAAGACATACACATA 2777451

QY 1381 ACGTGAGAGCATGTGCTATTCACCCGTAAGTGTGCTCTATTTTGAACGACGTG 1440
Db 2777450 ACGTGAGAGCATGTGCTATTCACCCGTAAGTGTGCTCTATTTTGAACGACGTG 2777391

QY 1441 CGGATTAAGATCGGTGTTTACTGTGATACCGCATGTCATGTGTCATGTCGAGGT 1500
Db 2777390 CGGATTAAGATCGGTGTTTACTGTGATACCGCATGTCATGTGTCGATGTCGAGGT 2777331

QY 1501 ACATGAGATCCGAGGAGGACGCGCATGTTGTGGTTCATTCGCCACGACAGATG 1560
Db 2777330 ACATGAGATCCGAGGAGGACGCGCATGTTGTGGTTCATTCGCCACGACAGATG 2777271

QY 1561 CTAAATGCTTGCCTCATGCGATGTGTCGCAAGTGTGATCGAAACCCGACGATGTC 1620
Db 2777270 CTAAATGCTTGCCTCATGCGATGTGTCGCAAGTGTGATCGAAACCCGACGATGTC 2777211

QY 1621 CGATGCTGCGATGCTGTTGGCATGCTGCTGGTGAAGCTTCGACCCGTTAAGTTC 1680
Db 2777210 CGATGCTGCGATGCTGTTGGCATGCTGCTGGTGAAGCTTCGACCCGTTAAGTTC 2777151

QY 1681 ACCAATTCGCTGAAGCTGTGTTTAAACACAGTTCTTTGGCATGTGAAGTTGG 1740
Db 2777150 ACCAATTCGCTGAAGCTGTGTTTAAACACAGTTCTTTGGCATGTGAAGTTGG 2777091

QY 1741 ACATGCTGTGAGGAGGACACCGAATTTGTATGACCATGAGGAAGTGAATTCGAG 1800
Db 2777090 ACATGCTGTGAGGAGGACACCGAATTTGTATGACCATGAGGAAGTGAATTCGAG 2777031

QY 1801 AGATTGCGCGCTCGGGTATCAATATGCTACGATACCGATCCGAAGTTCGCG 1860
Db 2777030 AGATTGCGCGCTCGGGTATCAATATGCTACGATACCGATCCGAAGTTCGCG 2776971

QY 1861 ACAGCTACTAGGATTTGCGATATCTGACCTGTACTGATGATATGTCACGATC 1920
Db 2776970 ACAGCTACTAGGATTTGCGATATCTGACCTGTACTGATGATATGTCACGATC 2776911

QY 1921 CTAAATGCTGTGACCCACACCATGATGAGGATGAGGATTCACAGG 1980
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	Query Match	80.4%;	Score 1737;	DB 10;	Length 1727;				
	Best Local Similarity	100.0%;	Pred. No. 0;						
	Matches 1737;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;				
QY	327	ATGCACACACGCTTACGCAGAACAACTTAATTGACACTTTGGAAAGCTCAAGGTGTGAGCGA	386						
Db	1	ATGCACACACACTTCGCGAGAACAACTTAATTGACACTTTGGAAAGCTCAAGGTGTGAGCGA	60						
QY	387	ATTATGAGTTTGGTGGTGAGCAGCCTTATCCGATCGGATGCTGTCGGCAATCAGAT	446						
Db	61	ATTATGAGTTTGGTGGTGAGCAGCCTTATCCGATCGTGAATGCTGTGTCGCCAATCAGAT	120						
QY	447	ATTGAGTGGGTGCACGTTCCGAATGAGSAGCGCGCGCTTGCACCCGTGCGGAATCG	506						
Db	121	ATTGAGTGGGTGCACGTTCCGAATGAGSAGCGCGCGCTTGCACCCGTGCGGAATCG	180						
QY	507	TTGATCACTGGGAGCTGCGAGTATGTGCTGCTTTTGAGTCCGGAATACACACCTG	566						
Db	181	TTGATCACTGGGAGCTGCGAGTATGTGCTGCTTTTGAGTCCGGAATACACACCTG	240						
QY	567	ATTGAGGCTCTTATGATTCGCATTCGGAATGGTGGGAAGGTGTGGCCATGCGTATGCCAT	626						
Db	241	ATTGAGGCTCTTATGATTCGCATTCGGAATGGTGGGAAGGTGTGGCCATGCGTATGCCAT	300						
QY	627	ATTCCGAGTGCACGATATGGTTTGCAGGTTCTTCCAGSAAAGCATCCGAGATTTTGTTT	686						

Db	301	ATTCCGAGTSCCCAGATTGGTTCCACAGTCTCTCCAGSAAACGATCCGGAGATTTTGT	360
Qy	687	AAGGAATGCTGTGGTTACTGCGAGATGGTAAATGTTGTTGAGCAGGGTGAACGATTTTG	746
Db	361	AAGGAATGCTGTGGTTACTGCGAGATGGTAAATGTTGTTGAGCAGGGTGAACGATTTTG	420
Qy	747	CATCAGCGGATTCAGTCCACCATGTCGGGGGTTAAAGTTGTCTCGGTGTAGTATTCCTGCT	806
Db	421	CATCAGCGGATTCAGTCCACCATGTCGGGGGTTAAAGTTGTCTCGGTGTAGTATTCCTGCT	480
Qy	807	GATTCGCGTAAGSAAAGACGACGAGTGACGGTACTTATTCGAAATTCGACTATTTCTTGCC	866
Db	481	GATATCGCTAAAGSAAAGACGACGAGTGACGGTACTTATTCGAAATTCGACTATTTCTTGCC	540
Qy	867	ACTCCTGTGTTGCCGAGTCTACTGAGGCTCCAGCGCTGTGAGAGGCGATTAAAC	926
Db	541	ACTCCTGTGTTGCCGAGTCTACTGAGGCTCCAGCGCTGTGAGAGGCGATTAAAC	600
Qy	927	GCTAAGTCTGCTACTTTGTTCTGGGGTCCGGGCGCTGAAGAAATGCTCCCGCCAGCTGTG	986
Db	601	GCTAAGTCTGCTACTTTGTTCTGGGGTCCGGGCGCTGAAGAAATGCTCCCGCCAGCTGTG	660
Qy	987	GAGTTGGCGGAGAGATTAAATCCACCATCGGCATCGCTGSGTGGTAACAGTACATC	1046
Db	661	GAGTTGGCGGAGAGATTAAATCCACCATCGGCATCGCTGSGTGGTAACAGTACATC	720
Qy	1047	CAGCATGAGATCCGTTTGAAGTGGCATGTCTGGCCTGCTTGGTTACGGGCTGTGCTG	1106
Db	721	CAGCATGAGATCCGTTTGAAGTGGCATGTCTGGCCTGCTTGGTTACGGGCTGTGCTG	780
Qy	1107	GATGCGTCCAAATGAGGCGGATCTGCTGATTTATTTGGTAAGGAAATTCCTTATTTGAT	1166
Db	781	GATGCGTCCAAATGAGGCGGATCTGCTGATTTATTTGGTAAGGAAATTCCTTATTTGAT	840
Qy	1167	TTCCTTCTTAAGAACAACGTTGCCAGGTGATATCAACGGTGGCGACATTTGTCGAGCT	1226
Db	841	TTCCTTCTTAAGAACAACGTTGCCAGGTGATATCAACGGTGGCGACATTTGTCGAGCT	900
Qy	1227	ACCAGGTGAGATTCGGGTGACCGGTGATGTTCTGCAACAATCGSAAATATTTGCT	1286
Db	901	ACCAGGTGAGATTCGGGTGACCGGTGATGTTCTGCAACAATCGSAAATATTTGCT	960
Qy	1287	CATGTGAAGSAAAAACAGATGTTCTCTCTTATGGAATGCTCAAGGCGCACAGAGCT	1346
Db	961	CATGTGAAGSAAAAACAGATGTTCTCTCTTATGGAATGCTCAAGGCGCACAGAGCT	1020
Qy	1347	AAAGTTGAGCTGGGTGTAGAGACGTACACACATTAACGTCCGAAGCATGTGCTTATTCAC	1406
Db	1021	AAAGTTGAGCTGGGTGTAGAGACGTACACACATTAACGTCCGAAGCATGTGCTTATTCAC	1080
Qy	1407	CCTGAATACGTGGCTCTATTTTAAACGAGTGGCGGGTAAGATAGCGGTTTACTGTG	1466
Db	1081	CCTGAATACGTGGCTCTATTTTAAACGAGTGGCGGGTAAGATAGCGGTTTACTGTG	1140
Qy	1467	GATACCGGCATGTGCATGTGTGSCATGCGATCGAATCGGAATCCGGAGGAACGCGC	1526
Db	1141	GATACCGGCATGTGCATGTGTGSCATGCGAGTACATCGAATCCGGAGGAACGCGC	1200
Qy	1527	GACTTTGGGTTTATTCGCCGACGAGCAGATGAGTGAATGGGTGGCCATGAGGATTTGTT	1586
Db	1201	GACTTTGGGTTTATTCGCCGACGAGCAGATGAGTGAATGGGTGGCCATGAGGATTTGTT	1260
Qy	1587	GCGCAAAGTGTGATCGAAACCGCCAGGTGATCCCGATGTGTGGCGATGTGTGTGGGC	1646
Db	1261	GCGCAAAGTGTGATCGAAACCGCCAGGTGATCCCGATGTGTGGCGATGTGTGTGGGC	1320
Qy	1647	ATGCTGCTGGGTGAGCTTCTGACCGTTAAAGTGTGACCAACTTCGCGCTGAAGCGTGTGTT	1706
Db	1321	ATGCTGCTGGGTGAGCTTCTGACCGTTAAAGTGTGACCAACTTCGCGCTGAAGCGTGTGTT	1380
Qy	1707	TTTAAACAACATTTCTTTGGGATGGTGAAGATGCTCGTGTGAGAGGACACCGCGAA	1766


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Db      61 ACATGCGGGAAGAGTGTGCGGTAGTATTCCTCGATATCGCTAAGGAGAC 120
Qy      825 GCAGGTGACGTAATTAATTCACAAATTCCTCTGCGACCTCTGTGTCCCG 884
Db      121 GCAGGTGACGTAATTAATTCACAAATTCCTCTGCGACCTCTGTGTCCCG 180
Qy      885 GATCCTACGAGGCTGCGAGCGGTGCGAGGATTAACAAGCTAAGCTGCTGCTTG 944
Db      181 GATCCTACGAGGCTGCGAGCGGTGCGAGGATTAACAAGCTAAGCTGCTGCTTG 240
Qy      945 TTCTGCGGTGCGGCGGTGAAGAATGCTCGCGGAGGTGTTGAGTTGCGGAGAGAT 1004
Db      241 TTCTGCGGTGCGGCGGTGAAGAATGCTCGCGGAGGTGTTGAGTTGCGGAGAGAT 300
Qy      1005 AATATCAGCATGCGGCGATGCGTGGTGGTAAAGCAGTACATCAGCATAGATCCGTTT 1064
Db      301 AATATCAGCATGCGGCGATGCGTGGTGGTAAAGCAGTACATCAGCATAGATCCGTTT 360
Qy      1065 GAGGTGCGATGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1124
Db      361 GAGGTGCGATGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
Qy      1125 GATCTGCTATTCATTAATGCGTAACGATTCCTTATTCGATTCCTTCTTAAAGCAAC 1184
Db      421 GATCTGCTATTCATTAATGCGTAACGATTCCTTATTCGATTCCTTCTTAAAGCAAC 480
Qy      1185 GTTGCCGAGTGGATATCAAGCGTGGGACATTTGGTGCAGTACCAAGGTGAAGTATCCG 1244
Db      481 GTTGCCGAGTGGATATCAAGCGTGGGACATTTGGTGCAGTACCAAGGTGAAGTATCCG 540
Qy      1245 GTGACCGGTGATGTTCTGTCACAAATCGAAATATTTGCTCATGTCGAAGAAAAACA 1304
Db      541 GTGACCGGTGATGTTCTGTCACAAATCGAAATATTTGCTCATGTCGAAGAAAAACA 600
Qy      1305 GATGCTTCCTTCCTTATGAGATGCTCAAGGACACAGAGTAAAGTGGTGGTGGTA 1364
Db      601 GATGCTTCCTTCCTTATGAGATGCTCAAGGACACAGAGTAAAGTGGTGGTGGTA 660
Qy      1365 GAGACGTACACATATACGTGCGAAGCATGTGCTTATTCACCTGTAATACGTGGCTCT 1424
Db      661 GAGACGTACACATATACGTGCGAAGCATGTGCTTATTCACCTGTAATACGTGGCTCT 720
Qy      1425 ATTGAACGAGTGGCGGATAAGATGGGCTTACTGATGATCCGCAATGTCAT 1484
Db      721 ATTGAACGAGTGGCGGATAAGATGGGCTTACTGATGATCCGCAATGTCAT 780
Qy      1485 GTGTGCGATGCGAGTACATCGAATTCGGAAGGAAACCGGACTTTGTGGTTCAATC 1544
Db      781 GTGTGCGATGCGAGTACATCGAATTCGGAAGGAAACCGGACTTTGTGGTTCAATC 840
Qy      1545 CGCCACGGCAGCATGCTAATGCTGCTCATGC 1579
Db      841 CGCCACGGCAGCATGCTAATGCTGCTCATGC 875

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RESULT 10

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US-10-143-856-5
; Sequence 5, Application US/10143856
; Publication No. US20030109014A1
; GENERAL INFORMATION:
; APPLICANT: BURKE, KEVIN
; APPLICANT: DUNICAN, L.K.
; APPLICANT: MCCORMACK, ASHLING
; APPLICANT: STRAPLETON, CLIONA
; APPLICANT: MCKEL, BETTINA
; APPLICANT: TRIERBACH, GEORG
; TITLE OF INVENTION: Process for the fermentative preparation of
; FILE REFERENCE: MAS/021123/282432
; CURRENT APPLICATION NUMBER: US/10/143,856
; PRIORITY FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/986,649

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; PRIOR FILING DATE: 17-03-2000
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 875
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-10-143-856-5

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Query Match      40.5%; Score 875; DB 14; Length 875;
Best Local Similarity 100.0%; Pred. No. 1.3e-277;
Matches 875; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      705 TGCGAGATGGAATGTTGGTGAAGGAGTGAAGCAATTTGATACAGCGCATTCAGCC 764
Db      1 TGCGAGATGGAATGTTGGTGAAGGAGTGAAGCAATTTGATACAGCGCATTCAGCC 60
Qy      765 ACCATGCGGGAAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 824
Db      61 ACCATGCGGGAAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
Qy      825 GCAGGTGACGTAATTAATTCACAAATTCCTCTGCGACCTCTGTGTCCCG 884
Db      121 GCAGGTGACGTAATTAATTCACAAATTCCTCTGCGACCTCTGTGTCCCG 180
Qy      885 GATCCTACGAGGCTGCGAGCGGTGCGAGGATTAACAAGCTAAGCTGCTGCTTG 944
Db      181 GATCCTACGAGGCTGCGAGCGGTGCGAGGATTAACAAGCTAAGCTGCTGCTTG 240
Qy      945 TTCTGCGGTGCGGCGGTGAAGAATGCTCGCGGAGGTGTTGAGTTGCGGAGAGAT 1004
Db      241 TTCTGCGGTGCGGCGGTGAAGAATGCTCGCGGAGGTGTTGAGTTGCGGAGAGAT 300
Qy      1005 AATATCAGCATGCGGCGATGCGTGGTGGTAAAGCAGTACATCAGCATAGATCCGTTT 1064
Db      301 AATATCAGCATGCGGCGATGCGTGGTGGTAAAGCAGTACATCAGCATAGATCCGTTT 360
Qy      1065 GAGGTGCGATGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1124
Db      361 GAGGTGCGATGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
Qy      1125 GATGCTTCCTTCCTTATGAGATGCTCAAGGACACAGAGTAAAGTGGTGGTGGTA 1184
Db      421 GATGCTTCCTTCCTTATGAGATGCTCAAGGACACAGAGTAAAGTGGTGGTGGTA 480
Qy      1185 GTTGCCGAGTGGATATCAAGCGTGGGACATTTGGTGCAGTACCAAGGTGAAGTATCCG 1244
Db      481 GTTGCCGAGTGGATATCAAGCGTGGGACATTTGGTGCAGTACCAAGGTGAAGTATCCG 540
Qy      1245 GTGACCGGTGATGTTCTGTCACAAATCGAAATATTTGCTCATGTCGAAGAAAAACA 1304
Db      541 GTGACCGGTGATGTTCTGTCACAAATCGAAATATTTGCTCATGTCGAAGAAAAACA 600
Qy      1305 GATGCTTCCTTCCTTATGAGATGCTCAAGGACACAGAGTAAAGTGGTGGTGGTA 1364
Db      601 GATGCTTCCTTCCTTATGAGATGCTCAAGGACACAGAGTAAAGTGGTGGTGGTA 660
Qy      1365 GAGACGTACACATATACGTGCGAAGCATGTGCTTATTCACCTGTAATACGTGGCTCT 1424
Db      661 GAGACGTACACATATACGTGCGAAGCATGTGCTTATTCACCTGTAATACGTGGCTCT 720
Qy      1425 ATTGAACGAGTGGCGGATAAGATGGGCTTACTGATGATCCGCAATGTCAT 1484
Db      721 ATTGAACGAGTGGCGGATAAGATGGGCTTACTGATGATCCGCAATGTCAT 780
Qy      1485 GTGTGCGATGCGAGTACATCGAATTCGGAAGGAAACCGGACTTTGTGGTTCAATC 1544
Db      781 GTGTGCGATGCGAGTACATCGAATTCGGAAGGAAACCGGACTTTGTGGTTCAATC 840
Qy      1545 CGCCACGGCAGCATGCTAATGCTGCTCATGC 1579
Db      841 CGCCACGGCAGCATGCTAATGCTGCTCATGC 875

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Db 2532155 CCCCTCAGAGATCGCCCTCGATTCCTCCAGSAGAACCCATCCGACGCTCTCCG 2532096
QY 689 GGAATGCTGTTGTTACTGCGAGATGTTGTAATGTTGTTGAGCAGAGTGAACGCAATTTTGA 748
Db 2532095 CGAGTGCATCTACTACGAGGAGATGATCTCCAAACCCGAAACGATATCCGAGCTGCTGCA 2532036
QY 749 TCACGGATTTCATCCACCATGGCGGGTAAAGTGTGTGCTGTGTAGTATTCCTGTGA 808
Db 2532035 GTCCGCAATCCAGCAGCAGCGGTGGTGTAGTCGCGTACAGCTGTCAACCTCCCGGCGA 2531976
QY 809 TATCGCTAAGAAAGACAGAGTACGCTACTTATTCCAATTCCTACTATTTCTCTGTGAC 868
Db 2531975 CGTCGCTCCGAGACCGCCCGGACAAAGCGCTCGAGACCGCCCTGTGACCTCCCGGCC 2531916
QY 869 TCCCTGTGTGTTCCCGGATCTCTACTAGCTGTGACGCTGTGTGAGGCGATTAAACAGC 928
Db 2531915 CACGGTCCGCGCCCGGCGA---CACCGAGATCGCAAGCTCTGTGCTGTGATCGACGCGC 2531859
QY 929 TAACTGTCTACTTTGTTGTGCGGTGCGGCGGTGAAGAAATGCTCGGCGGAGGTGTTGA 988
Db 2531858 CGACAAAGTCCACCTCTTTCTGCGGAGCGGCGACAGCGGCGGTGCGACGCGAGGTCAATGA 2531799
QY 989 GTTGGCGGAGAAAGATTAAATCAACCGATCGGCGATGCGGTGTAGTAAAGTATACCA 1048
Db 2531798 GTTCCGCCGAGAAAGATCAAGTCCCGGTGCGGACGCGGTGCGGCGCAAGAGTGTATCCA 2531739
QY 1049 GCATGAGAAATCCGTTTGAAGTGGGATGTCTGCGCTGCTGTGTTACGCGCCTGCTGGA 1108
Db 2531738 GTACGCAACCCGTCAGAGTGGGATGAGTGAGGCGCTCTCGGCTACGAGTCCGCTACGA 2531679
QY 1109 TCGTTCCAATGAGGCGGATCTCTGATTTCTATTTGGTACGSAATTCCTTATTCATTT 1168
Db 2531678 GGCACACAAAGATGGATCTGCTGATCTGCTGCGACCGACTTCCCGTACAAACGCTT 2531619
QY 1169 CCTTCTTA---AAGAACACGTTGCCAGGTGATATCAACGCTGCGACATGTGTGACG 1225
Db 2531618 CTTCCCAACCGATGTGAAGATGCAAGGTGACAGCTGACGCTCCCGGAACGCTGCGCGGG 2531559
QY 1226 TACCAAGGTGAGTATCCGCTGACCGGTATATGTTGCTGCAACAAATCGAAATATTTTGGC 1285
Db 2531558 CTCGAAGTTGACCTGCGCTGTGGGCGATGTGCGGAGACCTTCGCTGTATCC 2531499
QY 1286 TCATGTGAAGAAAAAAGACAGATGTTCTTCTTATGCGATGCTCAAGCAGCAGAGCG 1345
Db 2531498 GCGGGTGAAGCCCAAGAGAACCGGCGCTCTCCGACAAAGATGCTGAGAAAGCAGCGGA 2531439
QY 1346 TAACTTGAAGTGGGTGAGACGTACACATCAACCTCGAAGAAAGATGCTCTTATCA 1405
Db 2531438 CGCGCTCGAAGGTGTCATCAAGGCTTACACGCGGAAGGTGAGAAAGCAGTCCGATCCA 2531379
QY 1406 CCTGTAATACGTTGCTCTATTTTGAAGAGCTGGCGGATTAAGGATGCGGTCTTACTGT 1465
Db 2531378 CCGCGAGTACGTGGCTCTCGTCTGACGAACTGGCCGCGGAGAGCGGCTTTCACCGT 2531319
QY 1466 GGAATCCGCGATGTGCAATGTGTGCAATCGAGTACATCGAATCGAATCCGAGGAGACGCG 1525
Db 2531318 CGACACCGGAGATGTCAATGTGTGCGGCGCGCTACATCTG---CCCAAGGAGACGCGG 2531262
QY 1526 CGACTTGTGGTTCATTCCTCCGACAGCAGATGCTTAATGCGTTCATGCGATGCGATGG 1585
Db 2531261 CCGCGTCAATGCGCTGTCTTGTGCAAGCTTCAAGCGGCTTCCGATGGCGATGCGG 2531202
QY 1586 TCGCAAAAGTGTGATCGAAACCGCAGGTGATGCGCATGTTGGCGATGTTGGT 1645
Db 2531201 CGCCAGATTCACCGACCGGAAACCGGAGGTGCTCTCGATGTGCGGAGCGGAGTTCGCG 2531142
QY 1646 CATGCTGCTGGGTGAGCTTCTGACGTTAAGCTGACCAACTTCGCTGGAAGGCTGTGT 1705
Db 2531141 CATGCTGATGGGCACTCTCTACCCCTCGTCCAGTACGACGTGCCGGTGAAGTGTGACT 2531082
QY 1706 GTTTAAACAGAGTCTTTGGGCAATGTGAAGTGTGAGATGCTGCTGGAAGGACAGCCAGA 1765
Db 2531081 GTTCAACAACTCTCTTGAAGTGTGAGTGTGAGTGTGCGCGGCGTCCCTC 2531022
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QY 1766 ATTTGTACTGACCATGAGGAGTGAATTTTCGAGAGATTTCCGCGCTGCGGTATCA 1825
Db 2531021 GTACGGCACCAACGAAGAACCCGCACTTCGCGCGGTGCGCAGAGCGTGTGGCGCTA 2530962
QY 1826 ATGCGTACGATACCCATCCGAAAGATTCCGAGCAGCTAGCTAGGCAATTTGGCATA 1885
Db 2530961 CCGCGTGGCGGTGAGAGAGCCCAAGCAACTCGCGGCGCCTGAAGAGCGCTTCAGGA 2530902
QY 1886 TCCGTGACGCTGTACTGATTCATATTCGTCACGAGATCTTAATGCGTGTGATTCACCAAC 1945
Db 2530901 CAAGGACCGGCTCTGTCAATCATGTGACCGAGCCCAACGCTGTCTACCCGCGAA 2530842
QY 1946 CATCAGCTGGGAACAGGTCAATGGGATTACAGCAAGCGCGCAACCCGAAACGCTTTGGTGG 2005
Db 2530841 GATCAGCGCGGAGATGTTGAGCGGCTTCGCGCTGTCCGCTGAAATGTGCTGTGAGCG 2530782
QY 2006 AGAGATGAGAGCATGATTCATCTGCGCCGTTGCAACATAAGAAATATTCCTACTCAT 2064
Db 2530781 CCGGCTGCGCGGATGTGTGATGATGTCGCGCTCCACCTGCGAAGCTGCGCGCTCTT 2530723
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RESULT 13

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US-10-156-761-2067
; Sequence 2067, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 2067
; LENGTH: 1740
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; NAME/KEY: CDS
; LOCATION: (1)..(1740)
US-10-156-761-2067
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Query Match 24.2%; Score 522.6; DB 14; Length 1740;

Best Local Similarity 57.9%; Pred. No. 4.5e-161;

Matches 1006; Conservative 0; Mismatches 719; Indels 12; Gaps 4;

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QY 332 ACACAGCTACGAGAAATTAATGACATTTGGAAGCTCAAGGTGTGAAGGAATTTA 391
Db 9 ACAGAAACGTCGCGAGCAATTTGTGACATTCCTCCGCGGCGGCTCAATGCTGTGA 68
QY 392 TGGTTTGGTGGGTGACAGCTTAATCCATTCGTGATGCTGTCCGCC---AATCAGATAT 448
Db 69 CCGGGTGGTGGGTGACAGTCTCAACCCGCTGTCGACGCAATTCGCGCAACTCCGCAT 128
QY 449 TGAATGGGTGACGTTTCGAATGAGGAACCGCGGCTTTGACGCGGTGGGAAATGCTT 508
Db 129 CGACTGTGATCCAGTCGTCGAGAGGAGACCGCCGCTTTCGCGCGGCGGAGGCGGA 188
QY 509 GATCACTGGGAGCTGCGAGTATGTGCTCTTCTTGTGCTCGTGAACACACACACTGAT 568
Db 189 GATCACCGGCAAGCTTCGCGGCTGCGCGCTCTCTGCGGCGCCCGGAAACCTCAGCTCAT 248
QY 569 TCAGGCTCTTTATGATTCGATTCGAATGTGTGCGAAGGTGTTGGCCATCGCTAGCCATAT 628
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Db 249 CAACGGCTGTACAGCGCCACCGCTCCATGGCGCGGCTCCGCGCTCGCTCGCACAT 308
Qy 629 TCCGAGTCCCAAGATTGGTTCAGCTTCTTCCAGAAAACGATCCGAGATTTTGTAA 688
Db 309 CCCCCTCAGCGAGATCGGCTCGATCTTCCAGAGAACCCATCCCGACACACTCTTCG 368
Qy 689 GGAATGCTGTGGTCTGCGAGATGTGAATGTGTGAGCAAGGTTGAACGATTTTGA 748
Db 369 CGAGTGCAGTCACTACAGCGAGATGATCTCCAAACCGAAGAGATCCGAGGCTCTCA 428
Qy 749 TCAGCGATTCAATCCACCATGCGCGGTAAGGTGTGTGCGGTGAGTATGATTCCTGGA 808
Db 429 GTCCGCATCCAGACCGCGGTGGTCAATCCGCGCTCAGCGCTCGACCTCCCGGGA 488
Qy 809 TATGCTTAAGAAACGAGTGTACGCTATTATTCATTCATTCCTATTTCTTGGAC 868
Db 489 CGTGCTCCAGCGCGCGCGCGCGGACAAAGCGCGTGAACCGCTCTGATCCCGGCC 548
Qy 869 TCTGTGTGTTCCTCGATCTCTAGAGGTGACAGCGCTGTGTGAGGAGGATTAACAGC 928
Db 549 CACGCTCCGCGCGCGCGC---ACCGAGATGACAAAGCTCGTGGTGTATGACGCGC 605
Qy 929 TAACTGTGTCACTTTGTTCTGCGGTGCGGCGGTGAAGATCTGCGCGCAGGTGTGA 988
Db 606 CGACAGGTCAACCTCTTCTCGCGGACGCGGCGCGGCGGCGGACGCGGATGATGA 665
Qy 989 GTTGGCGAAGATTAATACAGCATGCGGCGGATGCGGTGGTGAAGCATATCA 1048
Db 666 GTTGGCGAAGATTAATCAAGTCCCGGTGCGGCGGCGGCGGCGGCGGCGGCGGCGG 725
Qy 1049 GCATGAGATCCGTTTGTGAGTGTGCGCATGTGCGGCTGTGTGATGCGGCGGCGTGA 1108
Db 726 GTAGACAAACCCGTACGCGTGGCGATGAGGCGGCTCTCGGCTACGCTGCGGCTTACGA 785
Qy 1109 TGGCTCAAGAGCGGATCTGCTGATTTCTATTGGTACGATTTCCCTTATTTGATTT 1168
Db 786 GGGCACCACAGAGTGTGCTGATCTGCTGCGGACGCGACTTCCGTTCAACGCTT 845
Qy 1169 CTTTCTA---AAGACAGGTTGCGGAGGTGATATCAAGGTGCGGACATGTGTCAGC 1225
Db 846 CTTGCCACCGATGTGAAGATCGACAGGTGCGGCTGCGGCGGCGGCGGCGGCGGCGG 905
Qy 1226 TACCAGGTGATGATCCGCTGACCGGTGATGTGTGCAACAATCCAAATATTTGCC 1285
Db 906 CTGGAAGTTGACCTCCCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 965
Qy 1286 TCATGGAAGAAAAACAGATGTTCTTCTTGTGATGCGATGCTCAAGCGACAGCGC 1345
Db 966 GCGGTTGAAGCCCAAGAGAACCGCGCTTCTCGAACAAGATGCTGAAGAACGCGGA 1025
Qy 1346 TAACTGAGCTCGGTAGAGAGTACACATTAACGTGAGAGATGCGCTATTTCA 1405
Db 1026 CCGGCTGAGAGGTGTCAAGGGGTACAGCGGAGAGTGTGAGAGACGCTTCGATCCA 1085
Qy 1406 CCGTGAATAGTTCCTCTATTTTTGAACGAGTGGCGGATAGAGATCGGTTTACTGT 1465
Db 1086 CCCCAGATGATGCTGCTGCTGCTGCAAGTGGCGCGGAGAGACGCGGTGTTACCGT 1145
Qy 1466 GATACCGGATGTGAATGTGTGCGATGAGGTGATGAGTGAATTCGAGAGAGCGC 1525
Db 1146 CGACACCGGATGTGAATGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1202
Qy 1526 CGACTTTGTGGTTCAATTCGCGCAGGAGATGCTTAATGCTTCTCATCGATTTG 1585
Db 1203 CCGGCTGATCAGGCTCTGCTGCGCAGCGCTCCATGGGAAAGCGCTCCGATGCGATCG 1262
Qy 1586 TGGGCAAGTGTGATGCAACCGCAGGTGATGCGGATGTGGCGATGTGTTGG 1645
Db 1263 CCGCCGTTTACCGACCGAGCGGAGTGTGCTGATGCTGCGGAGCGTGTGATTCG 1322
Qy 1646 CATGCTGTGTGAGCTTCTGACCTTAAGCTGACCAACTTCCCTGAAGGCTGTGGT 1705

Db 1323 CATGCTGATGGCGACTTCTTCAACCTCGTCCAGTACGACTGCGGTTGAAGTCTACT 1382
Qy 1706 GTTAAACAACAGTCTTTTGGCATGGTGAAGTTGAGATGCTGCGAGGACGACGAGA 1765
Db 1383 GTTCAACAACCTCTCTTGTAGCATGTGCAAGTTGAGATGCTGTGGCGGCTGCTTC 1442
Qy 1766 ATTTGCTACTGACCATGAGAGATGATTTTGCAGAGATTTGGCGGCTGCGGATCAA 1825
Db 1443 GTACGCGACACAGAACCAAGACCCGACTTTCGCGGCGCTGCGAGAGCTGTGGCGTA 1502
Qy 1826 ATCGGTAGCATCACCAGATCCCAAGAAATTTGCGAGCGCTAAGTGAAGCATTA 1885
Db 1503 CCGGCTGCGGCTGAGAAACCCAGCAACCTCCGCGGCGCTGAAAGAGCGCTTACGCA 1562
Qy 1886 TCTGTGACCTTACTGATGATGATGCTGATGATGCTGATGATGCTGATGATGATG 1945
Db 1563 CAAGGACCGCGCTCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1622
Qy 1946 CATCAGTGGGAACAGTCTATGAGATTCAGCAAGCGCGGCGGCGGCGGCGGCGG 2005
Db 1623 GATCAGCGCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1682
Qy 2006 AGGAGTAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2062
Db 1683 CCGGCTGCGGCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1739

RESULT 14
US-09-815-242-9898
Sequence 9898, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Cair, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA 0114
CURRENT APPLICATION NUMBER: US/09/815,242
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9898
LENGTH: 1719
TYPE: DNA
ORGANISM: Salmonella typhi
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1719)
US-09-815-242-9898

Query Match 16.0%; Score 344.8; DB 9; Length 1719;
Best Local Similarity 52.5%; Pred. No. 2.1e-102;
Matches 904; Conservative 0; Mismatches 797; Indels 21; Gaps 6;

327 ATGACACAGCGTACGACAGAACATTTATGACACTTTGGAGCTCAAGGTGACCGA 386
1 ATGAAACAAACCGTTGCTGCTTTATGCGCAAAACGCTGACACGCGTGCCTGCAAAACAA 60
387 ATTATGTTGGTGGGTGACAGCCTTAA--TCCGATCGGATGCTGTCCGCAATCA 443
61 ATCTGGGGGCTCACTGCGCAGCTCCCTGACAGCGCTGAGCCATCTTAAATCGATGGA 120
444 GATATTGAGTGGTGCACGTTGCAAAATGAGAAAGCGCGGCTTTGACGCGGTGCGAA 503
121 ACCATTGAATGGATGCCAACCCCGCACAGAGAGGTGCGCCCTTTGCGCGCGCGCAAA 180
504 TCGTTGATCAGCTGGGAGCTGGAGATATGCTGCTTCTTGCTGCTGGAACACACAC 563
181 GCGCAGCTTACCGCGAGCTGSCAGTGTGCGCGGTATTCATGTGACCGGCAACCTGAC 240
564 CTGATTCAGGCTCTTTATGATTCGATCGCAAAATGATGTCGAAAGTGTGGCATCGAGC 623
241 CTGATCAATGGCTGTTGATTTGCCACCGTAAACCGATCCCTGTTCTGGCGATCGCGCC 300
624 CATATTCGAGTCCCGAGATGTTGACGCTTTCAGAGAAACGATCCGAGATTTTG 683
301 CATATTCCGTCAGTAAATCGGACGCGTTATTCAGAGAGACCCACCGCAGAGGTG 360
684 TTTAAGGAATGCTCTGTTACTGTCGAGATGATGATGATGATGATGATGATGATGAT 743
361 TTCCGTAATGCGACCGCACTATTTGCGATGTTTCCAGCCCGGAGATCCGCGAGTA 420
744 TTGCAATCAGCGATTCAGTTCACCATGCGGCGTAAAGTGTGCGGTGATGATTTCT 803
421 CTGCGCATCGCATGCGCAAGAGGTGTAATCGCGCGCTCTCCGTGCGTACTTCCG 480
804 GGTGATATCGCTAAGGAACGAGGTGACGCTACTTATTCATTCATTCATTTCTTCT 863
481 GGTGAGTGGCGCTGAACCGCGGCTGAAACCGCGTCAACCATTTGTAACATGCCCCG 540
864 GGCATCTCTGTTGTTCCCGATCCTACTGAGGCTGCGACGCGTGTGAGAGGATTAAC 923
541 CAC---CCGCTGTTACGCGCGCGGAGGAAGAGCTGTAATAAATGCGCAATGCTGCC 597
924 AACGCTAAGTGTCACTTTGTTGCGGCTGCGGCGGTGAAGATCTCGCGCGCAGTG 983
598 TACTCCAGATATGCAATGATGATGCGGTAGCGGCTGCGCGCGCGCATGAGAGTTG 657
984 TTGAGTTGGCGGAGAGATTAATCACCAGTCGSCATGCGCTGGGTGTAACAGTAC 1043
658 GTGCGGTGGCGCAAACTAAAGCGCAATCGTTCATGCTGCGCGCAAGAGAC 717
1044 ATCCAGCATGAGATCCGTTTGAAGTGGCTGCGCTGCTGCTGCTGCTGCTGCTGCT 1103
718 GTTGAATGATTAACCCCTTATGATGAGGATGACCGGCTGATTTGCTTCTTCTG 777
1104 GTGGATGCGTCCATGAGCGGATGCTGCTGATTTATTGGGTACGAGATTTCCCTATT 1163
778 TTCCACACCATGATGACGCCCATGCTGATCTGCTGCGACCCAGTTCCCTATTCG 837
1164 GATTTCTTCTCTA---AAGACACGTTGGCCAGGATGATTAACGAGTCCGACATG 1220
838 GCTTTTATTCGAGGATGCGCAAAATCATTTAGATTGATGATCAACCCGCGCATTTG 897
1221 CGAGCTACACGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1280
898 GCGCAGACGAAGTGAATGAGCGCTGCTGCGCGGATTTAAAGCCACGCTTGGCGCGCT 957
1281 TTGCTCATGTGAAGAAAAACAGATGCTCTTCTGATGATGATGATGATGATGATGAT 1340
958 CTGCGCGTGTGAAGAAAAACAGATGCTCTTCTGATGATGATGATGATGATGATGAT 1014
1341 GAGCTAAGTGAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1400
1015 TATCGGACGCGCGGTAAGGCTTATGATGATGATGATGATGATGATGATGATGATGAT 1068

QY 1401 ATTACCTGATATGCTTGCCTTATTTTGAACGAGCTGGCGATTAAGATGCGTCTTT 1460
Db 1069 ATCCACCCCAATATCTGCGCACAACAAATATGATCTATTTGCGCGCTGACGAGCTATTTT 1128
QY 1461 ACTGTGATACCGCATGTGATATGCTGTGCGATGCGAGTACATGAGAAATCCGAGGGA 1520
Db 1129 ACTGCGATGTGCGCACCGCACCGTCTGGGGCGGCCGCTATCTAAAT--GAGCGC 1185
QY 1521 ACGCGCATTTTGGGTTCTATTCGCGCACGCGCATGATGATGATGATGATGATGATGAT 1580
Db 1186 AAGCGCGCTGCTGGGCTGCTTAAACCGAGGTCAATGCGCAACCGCATCCGTCGCGC 1245
QY 1581 ATTGTGCGCAAGTGTGATGCAACCGCAGGTGATGATGATGATGATGATGATGATGAT 1640
Db 1246 CTGCGCGCTGAGGCGCACCGCGCGGTGCTGATGATGATGATGATGATGATGATGATGAT 1305
QY 1641 TTGGGATGCTGCTGCGGTGAGCTTCTGACCGTTAAGCTGACCAACTTCCCTGAGGCT 1700
Db 1306 TTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1365
QY 1701 GTGCTTTTAAACACAGTTCTTTGGCATGATGATGATGATGATGATGATGATGATGAT 1760
Db 1366 GTGCTTTTAAATACAGCTGCTGCTGCTTGTGCGCATGGAATGAAGCTGCGGTAC 1425
QY 1761 CCAAGATTGCTACTGACCATGAGAGAGTGAATTCGCAAGATTCGCGCGCTGCGGCT 1820
Db 1426 CTTACCGACGCTACCGAATGCAACGACACCAATTTTCGCGCTATGCGCGAAGCTGCGGC 1485
QY 1821 ATCAAAATGCTAGCATCACCAGATCCCAAGAAATTTGCGGACGCTAGCTGAGCATTTG 1880
Db 1486 ATTACCGGATTTGCGCTGGAAGAACCGCAGACACTGAGCGAGCGCTAACACGCGCTTT 1545
QY 1881 GCATATCTGACCTGACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1940
Db 1546 TCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1605
QY 1941 CCAACATCACTGCGGACAGGTGATGATGATGATGATGATGATGATGATGATGATGAT 2000
Db 1606 CCGCAGATCAAACTGAAACAAGGAAAGGCTTATGCTGTAATGATGATGATGATGAT 1665
QY 2001 GGTGAGAGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 2042
Db 1666 AGCGCGCGCGCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1707

RESULT 15
US-09-965-825-12
; Sequence 12, Application US/09965825
; Patient No. US20020150999A1
; GENERAL INFORMATION:
; APPLICANT: DUSCH, Nicole
; APPLICANT: THOMAS, Herman
; APPLICANT: THIERBACH, Georg
; TITLE OF INVENTION: PROCESS FOR THE FERMENTATIVE PREPARATION OF D-PANTOTHENIC ACID
; TITLE OF INVENTION: CORYNEFORM BACTERIA
; FILE REFERENCE: 21354US0X
; CURRENT APPLICATION NUMBER: US/09/965,825
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: DE 10048604.5
; PRIOR FILING DATE: 2000-09-30
; PRIOR APPLICATION NUMBER: DE 10117085.8
; PRIOR FILING DATE: 2001-04-06
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 1422
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum

Query Match 15.0%; Score 324.4; DB 10; Length 1422;
Best Local Similarity 99.7%; Pred. No. 1e-95;
Matches 325; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 1 TTAGAGGCGATTCTGTGAGTCACTTTTGTGGGTCGCGGCTCTAATTGGCCAGTTT 60
    |||||||
Db 398 TTAGAGCGGATTCTGTGAGTCACTTTTGTGGGTCGCGGCTCTAATTGGCCAGTTT 457
    |||||||
OY 61 CGAGCGACACAGACAGGCGTGGCCACGATGTTAAATAGCGCGATCGGTGGCATCTGTGT 120
    |||||||
Db 458 CGAGCGACACAGACAGGCGTGGCCACGATGTTAAATAGCGCGATCTGTGT 517
    |||||||
OY 121 TTGGTTTGACGGGCTGAACCAACCAAGACTGCCAGCAACGACGAAATCCCAAAAGT 180
    |||||||
Db 518 TTGGTTTGACGGGCTGAACCAACCAAGACTGCCAGCAACGACGAAATCCCAAAAGT 577
    |||||||
OY 181 GGGCATCCCTGTTGTACCGAGTACCCACCCGGGCTGAAACTCCTGGCAGCGGGCG 240
    |||||||
Db 578 GGGCATCCCTGTTGTGTACCGAGTACCCACCCGGGCTGAAACTCCTGGCAGCGGGCG 637
    |||||||
OY 241 AAGCGTGGCAACACTGGAATTTAAGACACATGTAAGTGCACCAAGTTAGGCAACAC 300
    |||||||
Db 638 AAGCGTGGCAACACTGGAATTTAAGACACATGTAAGTGCACCAAGTTAGGCAACAC 697
    |||||||
OY 301 AATAGCCATAACGTTGAGGAGTTCAG 326
    |||||||
Db 698 AATAGCCATAAAGTTGAGGAGTTCAG 723
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Search completed: October 3, 2003, 21:08:46
Job time : 568 secs